

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: June 19, 2006, 09:00:06 ; Search time 50 Seconds  
(without alignments)  
693.243 Million cell updates/sec

Title: US-10-469-221-2

Perfect score: 2106

Sequence: 1 SQSQSPVPFPAPAPPQPP.....PLLLKRRKKARALEAAALAH 396

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /EMC Cellerai\_SIDS3/ptodata/2/iaa/5 COMB.pap.\*
- 2: /EMC Cellerai\_SIDS3/ptodata/2/iaa/6 COMB.pap.\*
- 3: /EMC Cellerai\_SIDS3/ptodata/2/iaa/7 COMB.pap.\*
- 4: /EMC Cellerai\_SIDS3/ptodata/2/iaa/H COMB.pap.\*
- 5: /EMC Cellerai\_SIDS3/ptodata/2/iaa/PCTUS COMB.pap.\*
- 6: /EMC Cellerai\_SIDS3/ptodata/2/iaa/RE COMB.pap.\*
- 7: /EMC Cellerai\_SIDS3/ptodata/2/iaa/backfiles1.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2106	100.0	400	2	US-09-538-092-1146
2	2076	98.6	396	2	US-09-142-551A-3
3	1854	88.0	370	2	US-09-142-551A-4
4	1391	66.0	382	2	US-09-142-551A-2
5	1391	66.0	382	2	US-09-949-016-6531
6	1391	66.0	396	2	US-09-949-016-11553
7	523	24.8	415	2	US-09-949-016-7462
8	523	24.8	370	1	US-08-878-989-19
9	512.5	24.3	370	2	US-09-272-796-19
10	512.5	24.3	370	2	US-09-457-040B-31
11	512.5	24.3	370	2	US-09-538-092-1314
12	499.5	23.7	355	2	US-09-579-664B-10
13	499.5	23.7	355	2	US-10-355-975A-10
14	499.5	23.7	355	3	US-09-980-464-10
15	498	23.6	476	2	US-09-960-643-2
16	498	23.6	385	2	US-09-733-388-2
17	496.5	23.6	385	2	US-10-446-175-2
18	493	23.4	356	2	US-09-733-388-4
19	493	23.4	356	2	US-10-446-175-4
20	493	23.4	356	2	US-09-538-092-1353
21	487.5	23.1	473	2	US-09-538-092-1178
22	486	23.1	740	2	US-09-771-161A-265
23	486	23.1	740	2	US-09-771-161A-266
24	486	23.1	740	2	US-08-715-568A-1
25	484.5	23.0	424	1	US-08-715-568A-1
26	474.5	22.5	358	2	US-09-230-896C-29

27	467	22.2	793	2	US-09-949-016-7810	Sequence 7810, Ap
28	464	22.0	639	2	US-09-347-801-17	Sequence 17, Appl
29	464	22.0	639	2	US-09-854-731-17	Sequence 17, Appl
30	458.5	21.8	424	2	US-09-771-161A-257	Sequence 257, App
31	458.5	21.8	424	2	US-09-771-161A-258	Sequence 258, App
32	458.5	21.8	424	2	US-09-771-161A-259	Sequence 259, App
33	454	21.6	463	1	US-07-951-715A-25	Sequence 25, Appl
34	454	21.6	463	1	US-08-459-448A-25	Sequence 25, Appl
35	454	21.6	463	2	US-08-459-595A-25	Sequence 25, Appl
36	454	21.6	463	2	US-08-459-504B-25	Sequence 25, Appl
37	454	21.6	463	2	US-08-459-444-25	Sequence 0, Appl
38	454	21.6	463	2	US-09-547-422-25	Sequence 0, Appl
39	454	21.6	463	2	US-09-988-462-25	Sequence 25, Appl
40	453.5	21.5	343	1	US-08-878-989-5	Sequence 5, Appl
41	453.5	21.5	343	2	US-09-272-796-5	Sequence 5, Appl
42	441	20.9	464	1	US-07-951-715A-22	Sequence 22, Appl
43	441	20.9	464	1	US-08-459-448A-22	Sequence 22, Appl
44	441	20.9	464	2	US-08-459-595A-22	Sequence 22, Appl
45	441	20.9	464	2	US-08-459-504B-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1

US-09-538-092-1146  
; Sequence 1146, Application US/09538092  
; Patent No. 6753314  
; GENERAL INFORMATION:  
; APPLICANT: Glot, Loic  
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same  
; FILE REFERENCE: 15966-542  
; CURRENT APPLICATION NUMBER: US/09/538,092  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: 60/127,352  
; PRIOR FILING DATE: 1999-04-01  
; PRIOR APPLICATION NUMBER: 60/178,965  
; PRIOR FILING DATE: 2000-02-01  
; NUMBER OF SEQ ID NOS: 1387  
; SOFTWARE: CurapatSeqFormatter Version 0.9  
; SEQ ID NO 1146  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (0)...(0)  
; OTHER INFORMATION: Polypeptide Accession Number P49137  
US-09-538-092-1146

Query Match	100.0%	Score 2106;	DB 2;	Length 400;
Best Local Similarity	100.0%;	Pred. No. 1.6e-159;	Indels 0;	Gaps 0;
Matches	396;	Conservative 0;	Mismatches 0;	
Qy	1	SQSQSPVPFPAPAPPQPPPTPALPHPPAQPPPPPPQPPQPPHVKSGLQIKKNAIDDKY 60		
Db	5	SQSQSPVPFPAPAPPQPPPTPALPHPPAQPPPPPPQPPQPPHVKSGLQIKKNAIDDKY 64		
Qy	61	VTSQVLGLGKINGKVLQIFNKRTQEKFPALQKMLQDCKPAREVELHWRASQCPHIVRVDVY 120		
Db	65	VTSQVLGLGKINGKVLQIFNKRTQEKFPALQKMLQDCKPAREVELHWRASQCPHIVRVDVY 124		
Qy	121	ENLYAGRKCLLIWMECLDGELFSRIQDRGQDQFTREASEIMKSGEALQYLHNSINIAH 180		
Db	125	ENLYAGRKCLLIWMECLDGELFSRIQDRGQDQFTREASEIMKSGEALQYLHNSINIAH 184		
Qy	181	RDVKPENLLYTSKRPNAILKLTDFGAKETTSNSLTTPCYTPYYVAPEVLGPEKDKSC 240		
Db	185	RDVKPENLLYTSKRPNAILKLTDFGAKETTSNSLTTPCYTPYYVAPEVLGPEKDKSC 244		
Qy	241	DMWSLGVIMVILLCGYPPPPVSNHGLAISPGMKTRIMGQYEFNPENWSEVSEVKMLRN 300		

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Db 245 DMWSLGVIMYILLCGYPPFYNSHGLAISPGMKTRIRMGQYEFNPNWSEVSEVKMLRN 304
Qy 301 LLKTEPTQRTMTITEFNMHPWIMOSTKVPQTPPLHSTRVLKEDKRWEDVKEMTSALATMR 360
Db 305 LLKTEPTQRTMTITEFNMHPWIMOSTKVPQTPPLHSTRVLKEDKRWEDVKEMTSALATMR 364
Qy 361 VDYEQIKKIKKIEDASNPILLKRRKKARALEAALAH 396
Db 365 VDYEQIKKIKKIEDASNPILLKRRKKARALEAALAH 400

RESULT 2
US-09-142-551A-3
; Sequence 3, Application US/09142551A
; Patent No. 6218136
; GENERAL INFORMATION:
; APPLICANT: KUMAR, SANJAY
; APPLICANT: LIVI, GEORGE P.
; APPLICANT: MCLAUGHLIN, MEGAN M.
; APPLICANT: YOUNG, PETER R.
; TITLE OF INVENTION: METHODS OF THE IDENTIFICATION OF
; FILE REFERENCE: P50448
; CURRENT APPLICATION NUMBER: US/09/142,551A
; CURRENT FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: PCT/US97/04256
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,286
; PRIOR FILING DATE: 1996-03-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-142-551A-3

Query Match 98.6%; Score 2076; DB 2; Length 396;
Best Local Similarity 99.0%; Pred. No. 3.7e-157;
Matches 392; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 SQQSPPVPFPAPAPPQPTPALPHPPAQPFPQFQFHVKSGLQIKKNAIIDDYK 60
Db 1 SQQSPPVPFPAPAPPQPTPALPHPPAQPFPQFQFHVKSGLQIKKNAIIDDYK 60
Qy 61 VTSQVLGLGINGKVLQIFNKRTQEKFKALQKMLQDCPKARREVELHWRASQCPHIVRVDVY 120
Db 61 VTSQVLGLGINGKVLQIFNKRTQEKFKALQKMLQDCPKARREVELHWRASQCPDVRVDVY 120
Qy 121 ENLYAGRKCLLIWMECLDGGELFSRIQDRGDAQFTEREASEIMKSGEAIQYLHSINIAH 180
Db 121 ENLYAGRKCLLIWMECLDGGELFSRIQDRGDAQFTEREASEIMKSGEAIQYLHSINIAH 180
Qy 181 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSNLSLTPCYTPYYVAPEVLGPEKDYKSC 240
Db 181 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSNLSLTPCYTPYYVAPEVLGPEKDYKSC 240
Qy 241 DMWSLGVIMYILLCGYPPFYNSHGLAISPGMKTRIRMGQYEFNPNWSEVSEVKMLRN 300
Db 241 DMWSLGVIMYILLCGYPPFYNSHGLAISPGMKTRIRMGQYEFNPNWSEVSEVKMLRN 300
Qy 301 LLKTEPTQRTMTITEFNMHPWIMOSTKVPQTPPLHSTRVLKEDKRWEDVKEMTSALATMR 360
Db 301 LLKTEPTQRTMTITEFNMHPWIMOSTKVPQTPPLHSTRVLKEDKRWEDVKEMTSALATMR 360
Qy 361 VDYEQIKKIKKIEDASNPILLKRRKKARALEAALAH 396
Db 361 VDYEQIKKIKKIEDASNPILLKRRKKARALEAALAH 396

RESULT 3
US-09-142-551A-4
; Sequence 4, Application US/09142551A
; Patent No. 6218136
; GENERAL INFORMATION:
; APPLICANT: KUMAR, SANJAY
; APPLICANT: LIVI, GEORGE P.
; APPLICANT: MCLAUGHLIN, MEGAN M.
; APPLICANT: YOUNG, PETER R.
; TITLE OF INVENTION: METHODS OF THE IDENTIFICATION OF
; FILE REFERENCE: P50448
; CURRENT APPLICATION NUMBER: US/09/142,551A
; CURRENT FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: PCT/US97/04256
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,286
; PRIOR FILING DATE: 1996-03-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-142-551A-4

Query Match 88.0%; Score 1854; DB 2; Length 370;
Best Local Similarity 99.1%; Pred. No. 1.6e-139;
Matches 346; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 SQQSPPVPFPAPAPPQPTPALPHPPAQPFPQFQFHVKSGLQIKKNAIIDDYK 60
Db 5 SQQSPPVPFPAPAPPQPTPALPHPPAQPFPQFQFHVKSGLQIKKNAIIDDYK 64
Qy 61 VTSQVLGLGINGKVLQIFNKRTQEKFKALQKMLQDCPKARREVELHWRASQCPHIVRVDVY 120
Db 65 VTSQVLGLGINGKVLQIFNKRTQEKFKALQKMLQDCPKARREVELHWRASQCPDVRVDVY 124
Qy 121 ENLYAGRKCLLIWMECLDGGELFSRIQDRGDAQFTEREASEIMKSGEAIQYLHSINIAH 180
Db 125 ENLYAGRKCLLIWMECLDGGELFSRIQDRGDAQFTEREASEIMKSGEAIQYLHSINIAH 184
Qy 181 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSNLSLTPCYTPYYVAPEVLGPEKDYKSC 240
Db 185 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSNLSLTPCYTPYYVAPEVLGPEKDYKSC 244
Qy 241 DMWSLGVIMYILLCGYPPFYNSHGLAISPGMKTRIRMGQYEFNPNWSEVSEVKMLRN 300
Db 245 DMWSLGVIMYILLCGYPPFYNSHGLAISPGMKTRIRMGQYEFNPNWSEVSEVKMLRN 304
Qy 301 LLKTEPTQRTMTITEFNMHPWIMOSTKVPQTPPLHSTRVLKEDKRWEDVK 349
Db 305 LLKTEPTQRTMTITEFNMHPWIMOSTKVPQTPPLHSTRVLKEDKRWEDVK 353

RESULT 4
US-09-142-551A-2
; Sequence 2, Application US/09142551A
; Patent No. 6218136
; GENERAL INFORMATION:
; APPLICANT: KUMAR, SANJAY
; APPLICANT: LIVI, GEORGE P.
; APPLICANT: MCLAUGHLIN, MEGAN M.
; APPLICANT: YOUNG, PETER R.
; TITLE OF INVENTION: METHODS OF THE IDENTIFICATION OF
; FILE REFERENCE: P50448
; CURRENT APPLICATION NUMBER: US/09/142,551A
; CURRENT FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: PCT/US97/04256
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,286
; PRIOR FILING DATE: 1996-03-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
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; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-142-551A-2

Query Match      66.0%; Score 1391; DB 2; Length 382;
Best Local Similarity 67.4%; Pred. No. 1.1e-102;
Matches 265; Conservative 50; Mismatches 56; Indels 22; Gaps 3;

Qy 1 SQQSPVPFPAPAPPQPPPTPALPHPPAQPAPPPPPQFPQFHVKSLQIKKNAIIDDYK 60
Db 6 AEEGGGVP-----PPVAPGGGLGGAPGGRREP-----KKYAVTDDYQ 44

Qy 61 VTSQVLGLGKLVQIFNKRTOEKFKALMLQDCPKARREVELHWRASQCPHIVRVDVY 120
Db 45 LSKQVLGLGVNGKVLCEFHRRITGQKALKLLYDSPKARQEVDDHHQASGGPHIVCILDVY 104

Qy 121 ENLYAGRKCLLIYMECLDGGELFSRIQDRGDAQFTEREASEIMKSIGEAIQYLHSHINIAH 180
Db 105 ENMHGKRCCLLIIMECMEGGELFSRIQERGDAQFTEREAAEIMRDIGTAIQLHSHINIAH 164

Qy 181 RDVKPENLLYTSKRPNAIKLTDGFAKETTSHNSLTTPCYTPYYVAPEVLGPEKYDKSC 240
Db 165 RDVKPENLLYTSKEKDAVLKLTDFGFAKETT-QNALQTPCYTPYYVAPEVLGPEKYDKSC 223

Qy 241 DMWSLGVIMYILLCGYPPFFYSNHLGLAISPGMKTRIRMGQYEFNPNPENSEVSEVKMLRN 300
Db 224 DMWSLGVIMYILLCGYPPFFYSNTGQAISPGMKRIRILGQYGFNPNPENSEVSEDAKQLIRL 283

Qy 301 LLKTEPTORMTITFEFNMHPWIMQSTKVPQTPPLHTSRVLKEDKERWEDVKEEMTSALATMR 360
Db 284 LLKTDPTERTLTITFNMHPWIMQSMVVPQTPPLHTARVLQEDKHDEKEDVKEEMTSALATMR 343

Qy 361 VDYEQIKIKKIEDASNPILLKRRKKARALEAAA 393
Db 344 VDYDQVKIKDLKTSNNRLLNKRKKQAGSSAS 376

RESULT 5
US-09-949-016-6531
; Sequence 6531, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6531
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6531

Query Match      66.0%; Score 1391; DB 2; Length 382;
Best Local Similarity 67.4%; Pred. No. 1.1e-102;
Matches 265; Conservative 50; Mismatches 56; Indels 22; Gaps 3;

Qy 1 SQQSPVPFPAPAPPQPPPTPALPHPPAQPAPPPPPQFPQFHVKSLQIKKNAIIDDYK 60
Db 6 AEEGGGVP-----PPVAPGGGLGGAPGGRREP-----KKYAVTDDYQ 44

Qy 61 VTSQVLGLGKLVQIFNKRTOEKFKALMLQDCPKARREVELHWRASQCPHIVRVDVY 120
Db 45 LSKQVLGLGVNGKVLCEFHRRITGQKALKLLYDSPKARQEVDDHHQASGGPHIVCILDVY 104

Qy 121 ENLYAGRKCLLIYMECLDGGELFSRIQDRGDAQFTEREASEIMKSIGEAIQYLHSHINIAH 180
Db 105 ENMHGKRCCLLIIMECMEGGELFSRIQERGDAQFTEREAAEIMRDIGTAIQLHSHINIAH 164

Qy 181 RDVKPENLLYTSKRPNAIKLTDGFAKETTSHNSLTTPCYTPYYVAPEVLGPEKYDKSC 240
Db 165 RDVKPENLLYTSKEKDAVLKLTDFGFAKETT-QNALQTPCYTPYYVAPEVLGPEKYDKSC 223

Qy 241 DMWSLGVIMYILLCGYPPFFYSNHLGLAISPGMKTRIRMGQYEFNPNPENSEVSEVKMLRN 300
Db 224 DMWSLGVIMYILLCGYPPFFYSNTGQAISPGMKRIRILGQYGFNPNPENSEVSEDAKQLIRL 283

Qy 301 LLKTEPTORMTITFEFNMHPWIMQSTKVPQTPPLHTSRVLKEDKERWEDVKEEMTSALATMR 360
Db 284 LLKTDPTERTLTITFNMHPWIMQSMVVPQTPPLHTARVLQEDKHDEKEDVKEEMTSALATMR 343

Qy 361 VDYEQIKIKKIEDASNPILLKRRKKARALEAAA 393
Db 344 VDYDQVKIKDLKTSNNRLLNKRKKQAGSSAS 376

RESULT 5
US-09-949-016-6531
; Sequence 6531, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6531
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6531

Query Match      66.0%; Score 1391; DB 2; Length 382;
Best Local Similarity 67.4%; Pred. No. 1.1e-102;
Matches 265; Conservative 50; Mismatches 56; Indels 22; Gaps 3;

Qy 1 SQQSPVPFPAPAPPQPPPTPALPHPPAQPAPPPPPQFPQFHVKSLQIKKNAIIDDYK 60
Db 6 AEEGGGVP-----PPVAPGGGLGGAPGGRREP-----KKYAVTDDYQ 44

Qy 61 VTSQVLGLGKLVQIFNKRTOEKFKALMLQDCPKARREVELHWRASQCPHIVRVDVY 120
Db 45 LSKQVLGLGVNGKVLCEFHRRITGQKALKLLYDSPKARQEVDDHHQASGGPHIVCILDVY 104

Qy 121 ENLYAGRKCLLIYMECLDGGELFSRIQDRGDAQFTEREASEIMKSIGEAIQYLHSHINIAH 180
Db 105 ENMHGKRCCLLIIMECMEGGELFSRIQERGDAQFTEREAAEIMRDIGTAIQLHSHINIAH 164

Qy 181 RDVKPENLLYTSKRPNAIKLTDGFAKETTSHNSLTTPCYTPYYVAPEVLGPEKYDKSC 240
Db 165 RDVKPENLLYTSKEKDAVLKLTDFGFAKETT-QNALQTPCYTPYYVAPEVLGPEKYDKSC 223

Qy 241 DMWSLGVIMYILLCGYPPFFYSNHLGLAISPGMKTRIRMGQYEFNPNPENSEVSEVKMLRN 300
Db 224 DMWSLGVIMYILLCGYPPFFYSNTGQAISPGMKRIRILGQYGFNPNPENSEVSEDAKQLIRL 297
Qy 301 LLKTEPTORMTITFEFNMHPWIMQSTKVPQTPPLHTSRVLKEDKERWEDVKEEMTSALATMR 360
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Db 45 LSKQVLGLGVNGKVLCEFHRRITGQKALKLLYDSPKARQEVDDHHQASGGPHIVCILDVY 104
Qy 121 ENLYAGRKCLLIYMECLDGGELFSRIQDRGDAQFTEREASEIMKSIGEAIQYLHSHINIAH 180
Db 105 ENMHGKRCCLLIIMECMEGGELFSRIQERGDAQFTEREAAEIMRDIGTAIQLHSHINIAH 164
Qy 181 RDVKPENLLYTSKRPNAIKLTDGFAKETTSHNSLTTPCYTPYYVAPEVLGPEKYDKSC 240
Db 165 RDVKPENLLYTSKEKDAVLKLTDFGFAKETT-QNALQTPCYTPYYVAPEVLGPEKYDKSC 223
Qy 241 DMWSLGVIMYILLCGYPPFFYSNHLGLAISPGMKTRIRMGQYEFNPNPENSEVSEVKMLRN 300
Db 224 DMWSLGVIMYILLCGYPPFFYSNTGQAISPGMKRIRILGQYGFNPNPENSEVSEDAKQLIRL 283
Qy 301 LLKTEPTORMTITFEFNMHPWIMQSTKVPQTPPLHTSRVLKEDKERWEDVKEEMTSALATMR 360
Db 284 LLKTDPTERTLTITFNMHPWIMQSMVVPQTPPLHTARVLQEDKHDEKEDVKEEMTSALATMR 343
Qy 361 VDYEQIKIKKIEDASNPILLKRRKKARALEAAA 393
Db 344 VDYDQVKIKDLKTSNNRLLNKRKKQAGSSAS 376

RESULT 6
US-09-949-016-11553
; Sequence 11553, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11553
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11553

Query Match      66.0%; Score 1391; DB 2; Length 396;
Best Local Similarity 67.4%; Pred. No. 1.2e-102;
Matches 265; Conservative 50; Mismatches 56; Indels 22; Gaps 3;

Qy 1 SQQSPVPFPAPAPPQPPPTPALPHPPAQPAPPPPPQFPQFHVKSLQIKKNAIIDDYK 60
Db 20 AEEGGGVP-----PPVAPGGGLGGAPGGRREP-----KKYAVTDDYQ 58

Qy 61 VTSQVLGLGKLVQIFNKRTOEKFKALMLQDCPKARREVELHWRASQCPHIVRVDVY 120
Db 59 LSKQVLGLGVNGKVLCEFHRRITGQKALKLLYDSPKARQEVDDHHQASGGPHIVCILDVY 118

Qy 121 ENLYAGRKCLLIYMECLDGGELFSRIQDRGDAQFTEREASEIMKSIGEAIQYLHSHINIAH 180
Db 119 ENMHGKRCCLLIIMECMEGGELFSRIQERGDAQFTEREAAEIMRDIGTAIQLHSHINIAH 178

Qy 181 RDVKPENLLYTSKRPNAIKLTDGFAKETTSHNSLTTPCYTPYYVAPEVLGPEKYDKSC 240
Db 179 RDVKPENLLYTSKEKDAVLKLTDFGFAKETT-QNALQTPCYTPYYVAPEVLGPEKYDKSC 237
Qy 241 DMWSLGVIMYILLCGYPPFFYSNHLGLAISPGMKTRIRMGQYEFNPNPENSEVSEVKMLRN 300
Db 238 DMWSLGVIMYILLCGYPPFFYSNTGQAISPGMKRIRILGQYGFNPNPENSEVSEDAKQLIRL 297
Qy 301 LLKTEPTORMTITFEFNMHPWIMQSTKVPQTPPLHTSRVLKEDKERWEDVKEEMTSALATMR 360
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Db	298	LLKTDPTLRTITQFMNHPWLNQSVVVPQTPLHTARVLQEDKDHDEKVEEMTSALATMR	357
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Db	358	VDYDQVKIKOLKTSNNLLNKKRRKKQAGSSSAS	390

RESULT 7

US-09-949-016-7461	
Sequence 7461, Application US/09949016	
Patent No. 6812339	
GENERAL INFORMATION:	
APPLICANT: VENTER, J. Craig et al.	
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED	
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF	
FILE REFERENCE: CL001307	
CURRENT APPLICATION NUMBER: US/09/949,016	
CURRENT FILING DATE: 2000-04-14	
PRIOR APPLICATION NUMBER: 60/241,755	
PRIOR FILING DATE: 2000-10-20	
PRIOR APPLICATION NUMBER: 60/237,768	
PRIOR FILING DATE: 2000-10-03	
PRIOR APPLICATION NUMBER: 60/231,498	
PRIOR FILING DATE: 2000-09-08	
NUMBER OF SEQ ID NOS: 207012	
SOFTWARE: FastSeq for Windows Version 4.0	
SEQ ID NO 7461	
LENGTH: 415	
TYPE: PRT	
ORGANISM: Human	
US-09-949-016-7461	

Query Match	24.8%;	Score 523;	DB 2;	Length 415;
Best Local Similarity	34.8%;	Pred. No. 1.5e-33;		
Matches 125;	Conservative 70;	Mismatches 126;	Indels 38;	Gaps 11;

Qy	18	QPPTPALPHPAQPPPPPPQPPHVSGLQIKNAIIDYKVTSSQVLGGLGKGVLIQI	77
Db	23	QPPRASQAPPRGALAVVGGQWAMLGAVGEPFWKQAEIRDIDYDFRDVLGTGAFSEVILA	82
Qy	78	FNKRTQSKFALKMLQDCPKARREVE-----LHWRASQCPHIVRIVDVVTENLYA	125
Db	83	EDKRTQKLVAIKCI-----AKEALEGEGSGMENEIAVLH--KIKHPNIVALDDIYES--G	133
Qy	126	GRKCLLIVMEGLDGEFLSRQDRGDQAFTEREASEIMKSIGEAICYLHLSINIAHRDVKP	185
Db	134	GH--LYLIMQVSGEFLDRIVEKG--FYTERDASRLIFQVLDAVKYLHDLCIVHRDLKP	189
Qy	186	ENLAYTSKRPNAILKLITDFGFAKETTSNLSITPCYTPYVAPEVLGPBKDYKSCDMWSL	245
Db	190	ENLLYLSLDEDSKIMISDFGLSKMEDPDGVSLSACGTGCVYVAPEVLAQPKPYSAVDCWSI	249
Qy	246	GVIMVILLCGYPFVSNHGLAISPGMKTRIRMGQVEFPNPESEVSEEVKMLIRLLKTE	305
Db	250	GVIAIYLLCGYPFPFYDENDAKLF----EQILKAEYEFDSPPYWDIDSASAKOPIRHLMEKD	305
Qy	306	PTQRMITTEFNHPIIMQSTKVPQTPFLH--TSRVLKED--KERWEDVKEEMTSALATMR	360
Db	306	PEKRTFCBQALQHPWIAAGDTALDKN-IHQSVSEQIKKNFAKSKW---KQAFNATAVVR	359

RESULT 8

US-09-949-016-7462	
Sequence 7462, Application US/09949016	
Patent No. 6812339	
GENERAL INFORMATION:	
APPLICANT: VENTER, J. Craig et al.	
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED	
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF	
FILE REFERENCE: CL001307	
CURRENT APPLICATION NUMBER: US/09/949,016	
CURRENT FILING DATE: 2000-04-14	



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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0321 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 370 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 790790
; US-08-878-989-19

Query Match 24.3%; Score 512.5; DB 1; Length 370;
Best Local Similarity 36.4%; Pred. No. 8.8e-33;
Matches 117; Conservative 68; Mismatches 95; Indels 41; Gaps 12;

Qy 56 IDYKVTQVLGLGKINGKVLQIFNKRTOEKFAKMLQDCPKARREVE-----L 103
Db 19 IYDFR---DVLGTGAFSEVILAEKRTQKLVAKICI-----AKEALEGKESMENEI AVL 70

Qy 104 HWRASQCPHIVRIVDVYENLYAGKCLLI VMECLDGGELFSRIODRGDQAFTEREASEIM 163
Db 71 H--KIKPNIVALDDIYES--GGH--LYLIMQLVSGGELFDRIVEKG--FYTERDASRLI 122

Qy 164 KSIGEALQYLHSINIAHRDVKPNLLYTSKRPNAILKLTDFGAKETTSNLSLTPCYTP 223
Db 123 FQVLDAVKYLHDLGI VHRDLKPNLLYSLDEDSKIMISDFGLSKMEDPGSVLSTACGTP 182

Qy 224 YVVAPEVLGPKEKYDKSCDMWSLGVIMYILLCGYPPFYNNHGLAISPGMKTRIRMGQYEPF 283
Db 183 GYVAPEVLAQPKYSAKVDWCWSIGVIAYILLCGYPPFYNDENDAKLF----EQILKAEYEF 238

Qy 284 NPWSEVSEVKMLIRNLKTEPTQRTMTITFNMHPWIMQSTKVPQTPPLH--TSRVLKED 341
Db 239 SPYWDIDSDSAKDFIRHLMKDPKRTCEQALQHPWIAGTDALDKN-IHQSVSEQIKKN 297

Qy 342 --KERWEDVKEEMTSALATMR 360
Db 298 FAKSKW----KQAFNATAVVR 314

RESULT 10
US-09-272-796-19
; Sequence 19, Application US/09272796
; Patent No. 6207148
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl G.
; APPLICANT: Lal, Preeti
; APPLICANT: Goli, Surya K.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
```

```
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/272,796
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/878,989
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0321 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 370 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 790790
; US-09-272-796-19

Query Match 24.3%; Score 512.5; DB 2; Length 370;
Best Local Similarity 36.4%; Pred. No. 8.8e-33;
Matches 117; Conservative 68; Mismatches 95; Indels 41; Gaps 12;

Qy 56 IDYKVTQVLGLGKINGKVLQIFNKRTOEKFAKMLQDCPKARREVE-----L 103
Db 19 IYDFR---DVLGTGAFSEVILAEKRTQKLVAKICI-----AKEALEGKESMENEI AVL 70

Qy 104 HWRASQCPHIVRIVDVYENLYAGKCLLI VMECLDGGELFSRIODRGDQAFTEREASEIM 163
Db 71 H--KIKPNIVALDDIYES--GGH--LYLIMQLVSGGELFDRIVEKG--FYTERDASRLI 122

Qy 164 KSIGEALQYLHSINIAHRDVKPNLLYTSKRPNAILKLTDFGAKETTSNLSLTPCYTP 223
Db 123 FQVLDAVKYLHDLGI VHRDLKPNLLYSLDEDSKIMISDFGLSKMEDPGSVLSTACGTP 182

Qy 224 YVVAPEVLGPKEKYDKSCDMWSLGVIMYILLCGYPPFYNNHGLAISPGMKTRIRMGQYEPF 283
Db 183 GYVAPEVLAQPKYSAKVDWCWSIGVIAYILLCGYPPFYNDENDAKLF----EQILKAEYEF 238

Qy 284 NPWSEVSEVKMLIRNLKTEPTQRTMTITFNMHPWIMQSTKVPQTPPLH--TSRVLKED 341
Db 239 SPYWDIDSDSAKDFIRHLMKDPKRTCEQALQHPWIAGTDALDKN-IHQSVSEQIKKN 297

Qy 342 --KERWEDVKEEMTSALATMR 360
Db 298 FAKSKW----KQAFNATAVVR 314

RESULT 11
US-09-457-040B-31
; Sequence 31, Application US/09457040B
; Patent No. 6387641
; GENERAL INFORMATION:
; APPLICANT: Vertex Pharmaceuticals Incorporated
; APPLICANT: Bellon, Steve
; TITLE OF INVENTION: Crystallized P38 Complexes
; FILE REFERENCE: VPI/98-14
; CURRENT APPLICATION NUMBER: US/09/457,040B
; CURRENT FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 41
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Patent No. 6759223  
; GENERAL INFORMATION:  
; APPLICANT: Immunex Corporation  
; APPLICANT: Bird, Timothy A.  
; APPLICANT: Virca, G. Duke  
; APPLICANT: Martin, Unja  
; APPLICANT: Anderson, Dirk M.  
; TITLE OF INVENTION: CALCIUM/CALMODULIN-DEPENDENT KINASE  
; FILE REFERENCE: 2923-B  
; CURRENT APPLICATION NUMBER: US/10/355,975A  
; CURRENT FILING DATE: 2003-01-30  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 10  
; LENGTH: 355  
; TYPE: PR1  
; ORGANISM: Mus musculus  
; US-10-355-975A-10

Query Match 23.7%; Score 499.5; DB 2; Length 355;  
Best Local Similarity 34.9%; Pred. No. 9.1e-32;  
Matches 119; Conservative 69; Mismatches 122; Indels 31; Gaps 11;

Qy 45 KSGLOIKKNAIIDDYKVTQSQVLGGLNGKVLQIFNKTQEFKALKMLQDCPKARREVELH 104  
Db 14 KQAEIDIKK---IFEFKET---LGTGAFSEVVLAEKATGKLFVAVKCPKKALKGKSSIE 67

Qy 105 -----WRASQCPHIVRIVDVYENLYAGRKCLLIWMECLDGGELFSRIQDRGDOAFTAREA 159  
Db 68 NEIAVLARKIHENITVALEDIYES-----PNHLYLVMLQVSGGELFDRIVEKG--FYTEKDA 121

Qy 160 SEIMKSIGEAIQYLHSINIAHRDVKPNLLYTSKRPNAILKLTDFGPAKETTSNLSLTP 219  
Db 122 STLIRQVLDAVYVLRMGIVHRDLKPNLLYSDDESKIMISDFGLSKMEGKGDVMSTA 181

Qy 220 CYTPYVVAPEVLGPEKYDKSCDMMSLGVIMVILLCGYPFYSNHGLAISPGMKTRIRMGQ 279  
Db 182 CGTPGYVAPEVLAQPKYSKAVDCWSIGVAYILLCGYPFYPDEN-----DSKLPFQILKAE 237

Qy 280 YEFNPPEWSEVSEVKMLIRNLKTEPTQRTMTITEFNNHPWIMQSTKVPQTPPLHTS---R 336  
Db 238 YEFDSPYWDIDSDSAKDFIRNLMEKDPNKRYTCEQAARHPWIAGDTALSKN-IHESVSAQ 296

Qy 337 VLKE-DKERWEDVKEEMTSALATMRVDYEQIKIKKIEDASN 376  
Db 297 IRKNFAKSKW----ROAFNATAVVR-HMRLQLGSSLDSSN 332

Search completed: June 19, 2006, 09:01:31  
Job time : 51 secs

RESULT 15  
US-09-980-464-10  
; Sequence 10, Application US/09980464  
; Patent No. 7001752  
; GENERAL INFORMATION:  
; APPLICANT: Immunex Corporation  
; APPLICANT: Bird, Timothy A.  
; APPLICANT: Virca, G. Duke  
; APPLICANT: Martin, Unja  
; APPLICANT: Anderson, Dirk M.  
; TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES  
; FILE REFERENCE: 2923-US  
; CURRENT APPLICATION NUMBER: US/09/980,464  
; CURRENT FILING DATE: 2001-11-27  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 10  
; LENGTH: 355  
; TYPE: PR1  
; ORGANISM: Mus musculus  
; US-09-980-464-10

Query Match 23.7%; Score 499.5; DB 3; Length 355;  
Best Local Similarity 34.9%; Pred. No. 9.1e-32;  
Matches 119; Conservative 69; Mismatches 122; Indels 31; Gaps 11;

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GenCore version 5.1.9  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 19, 2006, 14:43:31 ; Search time 7472 Seconds

(without alignments)  
5083.615 Million cell updates/sec

Title: US-10-469-221-2

Perfect score: 2106

Sequence: 1 SQGSPVPFPFAPAPPQPP.....PLLKRRKKARALEAALAH 396

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Fgapop 10.0 , Fgapext 0.5

Delop 6.0 , Delext 7.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
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8: gb\_sy.\*  
9: gb\_un.\*  
10: gb\_vi.\*  
11: gb\_ov.\*  
12: gb\_htg.\*  
13: gb\_in.\*  
14: gb\_cm.\*  
15: gb\_ba.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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1	2106	100.0	1690	5 BC036060	BC036060 Homo sapi
2	2106	100.0	2974	5 BC052584	BC052584 Homo sapi
3	2078	98.7	1336	2 AR380852	AR380852 Sequence

4	2078	98.7	1336	5 HSMAPKAP	X75346 H. sapiens m
5	1991.5	94.6	2258	2 AR270852	AR270852 Sequence
6	1991.5	94.6	2258	2 AX335055	AX335055 Sequence
7	1991.5	94.6	2258	5 HSU12773	U12773 Human MAP k
8	1931	91.7	2586	6 BC063064	BC063064 Mus muscu
9	1930	91.6	2862	6 BC062048	BC062048 Rattus no
10	1930	91.6	2909	6 AY197741	AY197741 Rattus no
11	1927	91.5	2604	6 BC052206	BC052206 Mus muscu
12	1921	91.2	1247	6 MMAPKAP	X76850 M. musculus
13	1764	83.8	1065	8 AY335730	AY335730 Synthetic
14	1729	82.1	1305	2 DD182194	DD182194 Methods a
15	1709	81.1	1168	2 CS214061	CS214061 Sequence
16	1709	81.1	1168	6 CLMAPKAP	X82220 C. longicaud
17	1689	80.2	2977	11 BC070986	BC070986 Xenopus l
18	1672	79.4	2786	11 CR761979	CR761979 Xenopus t
19	1663.5	79.0	2503	11 BC084300	BC084300 Xenopus l
20	1645	78.1	3265	11 BC054572	BC054572 Danio rer
21	1391	66.0	1149	8 AY335561	AY335561 Synthetic
22	1391	66.0	1149	8 AY892450	AY892450 Synthetic
23	1391	66.0	1149	8 AY892451	AY892451 Synthetic
24	1391	66.0	1149	8 BT008118	BT008118 Synthetic
25	1391	66.0	1298	5 HSU43784	U43784 Human mitog
26	1391	66.0	2481	2 AR270525	AR270525 Sequence
27	1391	66.0	2481	5 HSU09578	U09578 Homo sapien
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29	1391	66.0	2519	5 BC001662	BC001662 Homo sapi
30	1391	66.0	2523	5 BC010407	BC010407 Homo sapi
31	1377.5	65.4	2654	14 BC103321	BC103321 Bos tauru
32	1371	65.1	2634	6 BC081974	BC081974 Rattus no
33	1365	64.8	2484	2 CQ716382	Sequence
34	1361	64.6	2856	6 BC031467	BC031467 Mus muscu
35	1347	64.0	768	14 OCMAPKAP	X75345 O. cuniculus
36	1333	63.3	1333	2 AR145880	Sequence
37	1266	60.1	1544	13 DQ307182	DQ307182 Glossina
38	1243.5	59.0	2049	13 D82877	D82877 Hemiceutrot
39	1201	57.0	1982	13 DMU20757	U20757 Drosophila
40	1201	57.0	2000	2 CQ577905	Sequence
41	1201	57.0	2025	2 CQ601278	Sequence
42	1105	52.5	3949	13 AY069813	AY069813 Drosophil
43	1043	49.5	6276	2 CQ577904	Sequence
44	1043	49.5	6276	2 CQ601277	Sequence
45	1043	49.5	50394	12 AC014393	AC014393 Drosophil

## ALIGNMENTS

RESULT 1  
BC036060  
LOCUS  
DEFINITION

BC036060 1690 bp mRNA linear PRI 28-JUL-2005  
Homo sapiens mitogen-activated protein kinase-activated protein  
kinase 2, transcript variant 2, mRNA (cdna clone MGC:33670  
IMAGE:5296259), complete cds.

ACCESSION  
BC036060  
VERSION  
BC036060.1  
KEYWORDS  
MGC.  
SOURCE  
Homo sapiens (human)

ORGANISM  
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE  
AUTHORS

1 (bases 1 to 1690)  
Krauss, R.D., Collins, F.S., Wagner, L., Shennan, C.M., Schuler, G.D.,  
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,  
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,  
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,  
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,  
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,  
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,  
Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J.,  
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,  
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,  
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,









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Qy 281 GluPheProAsnProGluTyrPseXerGluValSerGluGluValLysMetLeuLeuArgAsn 300
Db 841 GAATTTCCCAACCCAGAGTGGTCAAGAGTATCAGAGGAGTGAAGATGCTCATTCGGAAT 900

Qy 301 LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTyr 320
Db 901 CTGTGTAACACAGAGCCACCCAGAGAGTACCATCACCAGATTTATGAACCAACCCCTGG 960

Qy 321 IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGlu 340
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Qy 341 AspLysGluArgTyrGluAspValLysGluGluMetThrSerAlaLeuAlaThrMetArg 360
Db 1021 GACAAGGAGCGGTGGAGGATGTCAAGAGGAGATGACCATGCTTGGCCACATCGCG 1080

Qy 361 ValAspTyrGluGlnIleLysIleLysLysIleGluAspAlaSerAsnProLeuLeuLeu 380
Db 1081 GTTGACTACGAGCAGATCAAGATAAAGATTGAAGATGATCATCAACCCCTCTGCTGCTG 1140

Qy 381 LysArgArgLysLysAlaArgAlaLeuGluAlaAlaLeuAlaHis 396
Db 1141 AAGAGCGGAAGAAGCTCGGGCCCTCGAGGCTCGCGCTTGGGCCAC 1188

RESULT 4
HSMAPKAP
LOCUS HSMAPKAP 1336 bp mRNA linear PRI 03-JAN-1994
DEFINITION H.sapiens mRNA for MAP kinase activated protein kinase.
ACCESSION X75346
VERSION X75346.1 GI:407074
KEYWORDS MAP kinase activated protein kinase-2; protein kinase.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 1336)
Stokoe,D., Caudwell,B., Cohen,P.T. and Cohen,P.
The substrate specificity and structure of mitogen-activated
protein (MAP) kinase-activated protein kinase-2
Biochem. J. 296 (Pt 3), 843-849 (1993)
8280084
REFERENCE 2 (bases 1 to 1336)
Stokoe,D.H.
Direct Submission
Submitted (30-SEP-1993) D.H. Stokoe, MRC Protein Phosphorylation
Unit, Dept of Biochemistry, Medical Sciences Institute, The
University of Dundee, Dundee DD1 4HN, United Kingdom
Location/Qualifiers
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/cell_line="NT9D1"
/clone_lib="lambda gt10"
/dev_stage="adult"
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/notes="serine and threonine-specific protein kinases which
generate phosphate esters (EC number group=2.7.10.X.)"
/codon_start=1
/product="MAP kinase activated protein kinase-2"
/protein_id="CAA53094.1"
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LHWASQCDIVIRVDYENLYAGKCLLIWMECLDGGELFSRIQDRGQOAPTEREAS
EIMKSGEALQVLSINIAHRVDYKPNAILYTSKRPNAILKLTDFGFAKETTSHNSLIT
PCYTPYVAPEVLGPKSKDSCMLVLGVMIYLLCGYPPFYNSHGLAISPMKTRIR
MGQYEPFNSEWSSEVSKMLIRNLKTEPTQMTITEFNMHPWIMQSTKVPOTPLHT
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CDS

## ALAH"

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ORIGIN
Alignment Scores: 3.18e-176 Length: 1336
Score: 2078.00 Matches: 393
Percent Similarity: 99.2% Conservative: 0
Best Local Similarity: 99.2% Mismatches: 3
Query Match: 98.7% Indels: 0
DB: 5 Gaps: 0

US-10-469-221-2 (1-396) x HSMAPKAP (1-1336)

Qy 1 SerGlnGlyGlnSerProProValProPheProAlaProAlaProProGlnProPro 20
Db 1 TCCAGGGCCAGAGCCCGCGGTTCCTCCGCCCGCCGCCGCCGCCGCCGCC 60

Qy 21 ThrProAlaLeuProHisProProAlaGlnProProProProGlnGlnPhePro 40
Db 61 ACCCTTGCCCTGCGCAGCCCGCGCGCAGCGCGCGCGCGCGCGCGCGCGCG 120

Qy 41 GlnPheHisValLysSerGlyLeuGlnIleLysLysAsnAlaIleIleAspAspTyrLys 60
Db 121 CAGTTCACGTCGAAGTCGGCCCTGCAGATCAAGAAGAACGCCCATCATCGATGACTACAAG 180

Qy 61 ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLys 80
Db 181 GTCCACAGCCAGGTCTCTGGGGCTGGGCATCAACGGCAAGTTTTCAGATCTTCAACAAG 240

Qy 81 ArgThrGlnGluLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaArgArgGlu 100
Db 241 AGGACCCAGGAGAAATTCGCCCTCAAAATGCTTTCAGACTGCCCAAGGCGCGCAGGAG 300

Qy 101 ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr 120
Db 301 GTGGAGCTGCACATGGCGGGCCCTCCAGTAGTCCCGCAGCATCGTACGGATCGTGTAC 360

Qy 121 GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly 140
Db 361 GAGAACTGTACGACGAGGAGGAGTGCCTGCTGATGTTCATGGAATGTTTGGCGGTGGA 420

Qy 141 GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer 160
Db 421 GAACTCTTTAGCCGAATCCAGGATCCAGGATCCAGGAGACAGGATTCACAGAAGAAGCATCC 480

Qy 161 GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis 180
Db 481 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCAATCAACATTGCCCAT 540

Qy 181 ArgAspValLysProGluAsnLeuTyrThrSerLysArgProAsnAlaIleLeuLys 200
Db 541 CGGGATGTCAAGCTCGAATCTCTTATACACCTCCAAAAGGCCCAACGCCATCCTGAAA 600

Qy 201 LeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCys 220
Db 601 CTCACATGACTTTGGCTTTCGAAGAAACCCAGGAGAACCCAGGACCAACATCTTTGACCACTCTGT 660

Qy 221 TyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys 240
Db 661 TATACACCTACTATGTGCTCCAGAAAGTCTGGGGTCCAGAGAAAGTATGCAAGTCTCTGT 720

Qy 241 AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProProPheTyr 260
Db 721 GACATGTTGGTCTCTGGGTGTTCATCATGATCATCTCTGTGTGGGTATCCCCCTCTCTAC 780

Qy 261 SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr 280
Db 781 TCCAAACCGGCTTCCCATCTCTCCGGGCATCAAGACTCGCATCCGAATCGGAATGGGCCAGTAT 840

Qy 281 GluPheProAsnProGluTyrPseXerGluValSerGluGluValLysMetLeuLeuArgAsn 300
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QY 301 LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTrp 320
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QY 321 IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGlu 340
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QY 341 AspLysGluArgTrpGluAspValLysGluLysMetThrSerAlaLeuAlaThrMetArg 360
Db 1021 GACAAGGAGCGGTGGGAGGATGCAAGGAGAGATGACCAAGTGCCTTGGCCACAATGGCG 1080
QY 361 ValAspTyrGluGlnIleLysLysLysLysLysLysLysLysLysLysLysLysLysLys 380
Db 1081 GTTGACTACGAGCAGATCAAGATAAAGATTGAAGATGCATCCAAACCCCTCTGCTGCTG 1140
QY 381 LysArgGlyLysAlaArgAlaLeuGluAlaAlaLeuAlaHis 396
Db 1141 AAGAGCGGAAGAAAGCTCGGGCCCTGGAGGCTGCGGCTCTGCCCCAC 1188

RESULT 5
LOCUS AR270852 2258 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 1415 from patent US 6500938.
ACCESSION AR270852
VERSION AR270852.1 GI:29702086
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2258)
AUTHORS Au-Young, J. and Seilhamer, J.J.
TITLE Composition for the detection of signaling pathway gene expression
JOURNAL Patent: US 6500938-A 1415 31-DEC-2002;
Incyte Genomics, Inc.; Palo Alto, CA;
WOX;

FEATURES
source Location/Qualifiers
1..2258
/organism="unknown"
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ORIGIN

Alignment Scores:
Pred. No.: 3,31e-168 Length: 2258
Score: 1991.50 Matches: 396
Percent Similarity: 69.0% Conservative: 0
Best Local Similarity: 69.0% Mismatches: 0
Query Match: 94.6% Indels: 178
DB: 2 Gaps: 1

US-10-469-221-2 (1-396) x AR270852 (1-2258)

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QY 21 ThrProAlaLeuProHisProProAlaGlnProProProProGlnGlnPhePro 40
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QY 41 GlnPheHisValLysSerGlyLeuGlnIleLysLysAsnAlaIleLeuAspTyrLys 60
Db 511 CAGTTCACGCTCAAGTCCGCGCTCGAGATCAAGAAAGCCCATCATCGATGACTACAAG 570
QY 61 ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLys 80
Db 571 GTCAACAGCCAGGTCCTGGGCTGGGCATCAACGGCAAGTTTTCAGATCTTCAACAAG 630
QY 81 ArgThrGlnGluLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaArgGlu 100
Db 631 AGGACCCAGGAGAAATTCGCGCTCAAAATGCTTCAGGACTGCCCGCAAGGCCCGAGGAG 690
QY 101 ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr 120

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QY 141 GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer 160
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QY 161 GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis 180
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Db 1111 GACATGTGTCCTGGGTGTCATCATGTATCATCTGCTGTGGGTATCCCGCTTCTAC 1170
QY 261 SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr 280
Db 1171 TCCAAACACCGGCTTCCCATCTCTCCGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 1230
QY 281 GluPheProAsnProGluTrpSerGluValSerGluGluValLysMetLeuIleArgAsn 300
Db 1231 GAATTTCCCAACCCAGAAATGGTCAGAAATGATCAGAGAAAGTGAAGATGCTCATTCGAAT 1290
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QY 349 349

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 Db 1891 TCTCTCACTGCTCTCTCTGCTGCTCTCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1950  
 QY 350 ----- GluGluMetThrSerAlaLeuAlaThrMetArgValAspTyr 363  
 Db 1951 GGTGCTGCGTGGCCCGCCAGGAGGAGATGACAGTGGCTTGGCCACAATGCGCGTTGACTA 2010  
 QY 363 rGluGlnIleLysIleLysIleGluAspAlaSerAsnProLeuLeuLysArgAr 383  
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 Db 2071 GAAGAAAGCTCGGGCCCTGGAGGCTGGCGCTTGGCCAC 2110

RESULT 6  
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 DEFINITION Sequence 5564 from Patent WO0194629.  
 ACCESSION AX335055  
 VERSION AX335055.1 GI:18125774  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.

REFERENCE  
 1 Young, P. E., Augustus, M., Carter, K. C., Ebner, R., Endress, G.,  
 Horrikan, S., Soppet, D. R. and Weaver, Z.  
 Cancer gene determination and therapeutic screening using signature  
 gene sets  
 JOURNAL Patent: WO 0194629-A 5564 13-DEC-2001;  
 Avalon Pharmaceuticals (US)  
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 source 1..2258  
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ORIGIN  
 Alignment Scores:  
 Pred. No.: 3,31e-168 Length: 2258  
 Score: 1991.50 Matches: 396  
 Percent Similarity: 69.0% Conservative: 0  
 Best Local Similarity: 69.0% Mismatches: 0  
 Query Match: 94.6% Indels: 178  
 DB: 2 Gaps: 1

US-10-469-221-2 (1-396) x AX335055 (1-2258)

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 Db 391 TCCAGGGCCAGAGCCCGCGTGGTCCGTTCCCGCCCGCGCGCGCGCGCGCGCGCGCGCGCG 450  
 QY 21 ThrProAlaLeuProHisProAlaGlnProProProProProGlnGlnPhePro 40  
 Db 451 ACCCTGCGCTGCGCGACCCCG 510  
 QY 41 GlnPheHisValLysSerGlyLeuGlnIleLysLysAsnAlaIleLeuAspTyrLys 60  
 Db 511 CAGTTCACGCTCAAGTCCGGCTCGAGATCAAGAAAGCCCATCATCGATGACTACAAG 570  
 QY 61 ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLys 80  
 Db 571 GTCAACGCCAGGCTCTGGGGCTGGGCATCAACGGCAAGTTTTCGATCTCTGCGCCCAAGT 630

QY 81 ArgThrGlnGluLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaAraArgGlu 100  
 Db 631 AGACCCAGGAGAAATTCGCCCTCAAAATGCTTCAGGACTGCCCAAGGCCCGCAGGGAG 690  
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 Db 1111 GATATGTGTCCTGGGTGTCATCATCTGCTGCTGGGTATCCCGCTCTCTAC 1170  
 QY 261 SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr 280  
 Db 1171 TCCAAACCCGCGCTTGGCATCTCTCGGGCATGAGACTCGCATCCGAATGGGCCAGTAT 1230  
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 Db 1351 ATCATGCAATCAACAAAGTTCCTCAACCCCACTGCACACCGCGCGTCTTGAAGGAG 1410  
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Qy	350	-----GluGluMetThrSerAlaLeuAlaThrMetArgValaAspTY	363
Db	1951	GGTGCTGCCGTGCCCCACGAGGAGATGACCAAGTCCCTTGGCCACAATGCCGTTGACTA	2010
Qy	363	rGluGlnIleIysIleIysIleGluAspAlaSerAsnProLeuLeuLeuIysArgAr	383
Db	2011	CGAGCAGATCAAGATAAATAAGATTGAAGATGCATCAACCTCTGCTGCTGAAGAGCG	2070
Qy	383	qLysLYAlaArgAlaLeuGluAlaAlaAlaLeuAlaHis	396
Db	2071	GAAGAAAGTCGGCCCTGGAGGCTCGGCTCTGGCCAC	2110
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LOCUS	Human MAP kinase activated protein kinase 2 mRNA, complete cds.		
DEFINITION	U12779		
ACCESSION	U12779.1	GI:530089	
VERSION			
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
LOCUS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
DEFINITION	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
ACCESSION	Hominidae; Homo.		
VERSION	1 (bases 1 to 2258)		
KEYWORDS	Zu, Y.L., Wu, F., Gilchrist, A., Ai, Y., Labadia, M.E. and Huang, C.K.		
SOURCE	The primary structure of a human MAP kinase activated protein kinase 2		
ORGANISM	Biochem. Biophys. Res. Commun. 200 (2), 1118-1124 (1994)		
LOCUS	8179591		
DEFINITION	2 (bases 1 to 2258)		
ACCESSION	Huang, C.		
VERSION	Direct Submission		
KEYWORDS	Submitted (29-JUL-1994) Chi-Kuang Huang, Pathology, University of Connecticut Health Center, 263 Farmington Ave., Farmington, CT 06030, USA		
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SOURCE	REASEINKTSGEAIPQIYLHSINIAHRDVKPENLIYSKRPNAILLKIDFGPAKETS		
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ACCESSION	TRRMGQYEPNPWSVSEVKMLIRNLKLTPTQMTITEFMNHPWIMQSTKVPQT		
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SOURCE			
ORIGIN			

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Db 1411 GACAAGGAGCGGTGGGAGGATGCTCAAGGGGTGTCTTCATGACAAGAACAGCGACGAGGCC 1470
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Qy 349 ----- 349
Db 1471 ACTTGGCTGACCAGGTTGTGACAGAGGATTCTGTGTTCTGTCCTCAAACTCAGTGTGTT 1530
|||
Qy 349 ----- 349
Db 1531 TCTTAGAATCCTTTTATTCCCTGGTCTCTAATGGACCTTAAGACCATCTGGTATCAT 1590
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Qy 349 ----- 349
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Qy 349 ----- 349
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Qy 350 -----GluMetThrSerAlaLeuAlaThrMetArgValAspTy 363
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RESULT 8
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LOCUS Mus musculus MAP kinase-activated protein kinase 2, mRNA (cdna
DEFINITION clone MGC:67217 IMAGE:5687007), complete cds.
ACCESSION BC063064
VERSION BC063064.1 GI:38969982
KEYWORDS MGC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
1 (bases 1 to 2586)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Schetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Vallalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahy,J., Helton,E., Kettman,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalios,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 2586)
Strausberg,R.
Direct Submission
Submitted (02-DEC-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: M. Bento Soares, University of Iowa
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcsc.bc.ca
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth
Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,
Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu,
Parvaneh Saeedi, JR Stott, Angelique Schnerch, Ursula Skalska,
Duane Smalios, Jeff Stott, Miranda Tsai, George Yang, Jacque
Schein, Asim Siddiqui, Rob Holt, Marco Marra.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/ILNL at: http://image.llnl.gov
Series: IRAC Plate: 124 Row: b Column: 6
This clone was selected for full length sequencing because it
passed the following selection criteria: Similarity but not
identity to protein.
FEATURES
Location/Qualifiers
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## ORIGIN

## Alignment Scores:

Pred. No.: 1.02e-162 Length: 2586  
Score: 1931.00 Matches: 368  
Percent Similarity: 94.7% Conservative: 7  
Best Local Similarity: 92.9% Mismatches: 7  
Query Match: 91.7% Indels: 14  
DB: 6 Gaps: 2

US-10-469-221-2 (1-396) x BC063064 (1-2586)

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DB	79	-----GCCCGGCCCGCCAGCGCGCGCGCG-----TTCCCC	108
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DB	109	CAGFTTCCAGCTGCAAGTCGGGCGCTGCAGATCCGAAAGAACGCCATCACCGACGACTACAAG	168
QY	61	ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnInleIlePheAsnLys	80
DB	169	GTACACAGCCCAAGTCTGGCCTGGGCATCAACGGGAAGGTGCTGCGGATCTTCGACAAG	228
QY	81	ArgThrGlnGlyLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaArgArgGlu	100
DB	229	AGAACCCAGCAAAATTCGCCCTAAAGATGCTCCAGGACTGTCCGAAGGCGCGCAGAGAG	288
QY	101	ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr	120
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QY	121	GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly	140
DB	349	GAGNACTGTATGCGGGAGGAGTGCCTGCTGATTCTCATGGATGCTTCGATGGTGA	408
QY	141	GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer	160
DB	409	GAGCTCTTTAGTCGAATCCAGGACCGAGGAGACCGAGCAATTCACAGAAAGAGAGCGCTCA	468
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QY	181	ArgAspValLysProGluAsnLeuTyrThrSerLysArgProAsnAlaIleLeuLys	200
DB	529	CGGGATGCAAGCTTGAGACCTCTTATATCTTCCAAAGGCCCAATGCAATTTTGAAA	588
QY	201	LeuThrAspPheGlyPheAlaLysGluThrThrSerHisSerLeuThrThrProCys	220
DB	589	CTCACTGATTTTGGCTTTGGCCAGGAAACCCAGTCAGTCCACAACTCTTTTGACCACTCCCGTGT	648
QY	221	TyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys	240
DB	649	TATACACCATACTATGTGGCTCCGGAAGTCTGGGCGCCGGAGAGTATGACAGTCTCTGT	708
QY	241	AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProProPheTyr	260
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QY	261	SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr	280
DB	769	TCCAATCAGCGCCTTGCCATCTCTCCGGGATGAAGACTCGTATTCGAATGGGCGCAGTAT	828

QY	281	GluPheProAsnProGluTrpSerGluValSerGluGluValLysMetLeuIleArgAsn	300
DB	829	GAATTTCCTAAACCCGAGTGGTCAGAAAGTATCAGAAAGAGTGAAGATGCTTATCCCGAAT	888
QY	301	LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTyr	320
DB	889	CTGCTAAAACACAGAGCCACCCAGAGATGACCATCACAGATTCATGAACACCCCTGG	948
QY	321	IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGlu	340
DB	949	ATCATGCAATCTACGAAGGTCCCTCAGACTCCACTGCACACACGCGCTGTCTCGAAGGAG	1008
QY	341	AspLysGluArgTrpGluAspValLysGluGluMetThrSerAlaLeuAlaThrMetArg	360
DB	1009	GACAAGGACGATGGGAGGATGTCAAGGAGGAGATCACCAGTCCCTTGGCCAGATGCGT	1068
QY	361	ValAspTyrGluGlnIleLysIleLysIleGluAspAlaSerAsnProLeuLeuLeu	380
DB	1069	GTGTGACTATGACGAGATCAAGATAAAGAGATAGAGACGATCCCAACCCCTGCTCTCTC	1128
QY	381	LysArgArgLysLysAlaArgAlaLeuGluAlaAlaLeuAlaHis	396
DB	1129	AAGAGCGGAAGAAAGCTCGTGTGTGGAGATGCGGCTCTCGCCAC	1176

## RESULT 9

BC062048

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Rattus norvegicus (Norway rat)

Rattus norvegicus

Eukaryota; Metazoa

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidae; Murinae; Rattus.

1 (bases 1 to 2862)

Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,

Klausner,R.D., Collins,F.S., Wagner,L., Shennen,C.M., Schuler,G.D.,

Altshul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,

Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,

Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,

Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,

Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S,

Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,

Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,

McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,

Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,

Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,

Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S.,

Sanchez,A., Whitting,M., Madan,A., Young,A.C., Shevchenko,Y.,

Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,

Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,

Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalish,D.E.,

Schneerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932

2 (bases 1 to 2862)

Strausberg,R.

Direct Submission

Submitted (10-NOV-2003) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: <http://mgc.ncbi.nlm.nih.gov>

Contact: MGC help desk

Email: [cgabbs@mail.nih.gov](mailto:cgabbs@mail.nih.gov)

Tissue Procurement: Jeff Green/Paturu Kondaiah, NCI.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC),  
Gaithersburg, Maryland;  
Web site: <http://www.nisc.nih.gov/>  
Contact: [nisc\\_mgc@nigr1.nih.gov](mailto:nisc_mgc@nigr1.nih.gov)  
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,  
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,  
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,  
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,  
Maduro, O.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,  
McDowell, J., Pearson, R., Stantropop, S., Thomas, P.J., Touchman, J.W.,  
Tsurgon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,  
Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAP Plate: 137 Row: b Column: 22  
This clone was selected for full length sequencing because it  
passed the following selection criteria: matched mRNA gi: 31342499.

## FEATURES

Location/Qualifiers  
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## ORIGIN

Alignment Scores:  
Pred. No.: 1.41e-162 Length: 2862  
Score: 1930.00 Matches: 367  
Percent Similarity: 94.7% Conservative: 8  
Best Local Similarity: 92.7% Mismatches: 7  
Query Match: 91.6% Indels: 14  
DB: 6 Gaps: 2

US-10-469-221-2 (1-396) x BC062048 (1-2862)

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Db 328 -----GCCCGCGCCAGCGCGCGCGCG-----TTCCT 357  
Qy 41 GlnPheHisValLysSerGlyLeuGlnLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 60  
Db 358 CAGTTCACGCTCAAGTCGGGCGCTCGATCCGAAAGAACGCCATCACCGACGACTCAAG 417

Qy 61 ValThrSerGlnValLeuGlyLeuGlyLeuGlyLeuGlyLeuGlyLeuGlyLeuGlyLeu 80  
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## RESULT 10

AY197741

LOCUS

DEFINITION

AV197741

2909 bp mRNA linear

ROD 02-MAR-2003

Rattus norvegicus mitogen-activated protein kinase-activated

protein kinase-2 mRNA, complete cds.

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ACCESSION AV197741
VERSION AV197741.1 GI:28629390
KEYWORDS
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
          Sciurognathi; Muridae; Muridae; Muridae; Rattus.
REFERENCE 1 (bases 1 to 2909)
AUTHORS Vician, L.J., Xu, G., Liu, W., Feldman, J.D., Machado, H.B. and
        Herschman, H.R.
TITLE MAPKAP Kinase-2 is a Primary Response Gene Induced by
        Depolarization in PC12 Cells and in Brain
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2909)
AUTHORS Vician, L.J., Xu, G. and Herschman, H.R.
TITLE Direct Submission
JOURNAL Submitted (16-DEC-2002) Biological Chemistry, UCLA, 611 Charles E.
        Young Dr. East, Los Angeles, CA 90095-1570, USA
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3' UTR
ORIGIN
Alignment Scores:
Pred. No.: 1.44e-162 Length: 2909
Score: 1930.00 Matches: 367
Percent Similarity: 94.7% Conservatives: 8
Best Local Similarity: 92.7% Mismatches: 7
Query Match: 91.6% Indels: 14
DB: Gaps: 2

US-10-469-221-2 (1-396) x AV197741 (1-2909)
Qy 1 SerGlnGlnSerProValProPheProAlaProAlaProProGlnProPro 20
Db 314 TCTCCGGGCCAGACTCGCGCGCGCGTTCGCCAGCGCCGCCACCC----- 361
Qy 21 ThrProAlaLeuProHisProProAlaGlnProProProProGlnGlnPhePro 40
Db 362 -----GCCCGCGCCAGCGCGCGCGCG-----TTCCT 391
Qy 41 GlnPheHisValLysSerGlyLeuGlnIleLysLysAsnAlaIleLeuAspTyrLys 60
Db 392 CAGTTCACGTCAGTTCGGGCTCGAGTCCGAAGAAGCCCATCCAGCAGCTACAAG 451
Qy 61 ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLys 80
Db 452 GTCAACCGCCAGTGTGCTGGCTGGCATCAACGGGAAGGTGCTGCGGATCTTCGCAAG 511

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RESULT 11  
BC052206/c  
LOCUS  
DEFINITION Mus musculus cDNA clone IMAGE:6432632.  
ACCESSION BC052206  
VERSION BC052206.1 GI:30354049  
KEYWORDS Mus musculus (house mouse)  
SOURCE Mus musculus  
ORGANISM

BC052206 2604 bp mRNA linear ROD 06-JUN-2005  
IMAGE:6432632.



REFERENCE AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. 1 (bases 1 to 2604) Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeb,B., Moore,T., Max,S.I., Wang,J., Hsieh,F., Hopkins,R.F., Jordan,H., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Diatchenko,L., Marusik,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Schetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullany,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A., Young,A.C., Shevchenko,Y., Sanchez,A., Whiting,M., Madao,A., Touchman,J.W., Green,E.D., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalhus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A. Mammalian Gene Collection Program Team Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) 12477932 2 (bases 1 to 2604)
CONSRMT TITLE	NIH MGC Project Direct Submission Submitted (01-MAY-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a> Contact: MGC help desk Email: <a href="mailto:cgabs-remail.nih.gov">cgabs-remail.nih.gov</a> Tissue Procurement: Gerard Gradwohl (PNAS 97 P1607-1611, 2000) cDNA Library Preparation: Catherine Lee, Endocrine Pancreas Consortium cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center Center code: BCM-HGSC Web site: <a href="http://www.hgsc.bcm.tmc.edu/cdna/">http://www.hgsc.bcm.tmc.edu/cdna/</a> Contact: <a href="mailto:amg@bcm.tmc.edu">amg@bcm.tmc.edu</a> Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.
REMARK COMMENT	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Series: IRAK Plate: 111 Row: b Column: 12 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 45544579. Location/Qualifiers 1. .2604 /organism="Mus musculus" /mol_type="mRNA" /db_xref="taxon:10090" /clone="IMAGE:6432632" /tissue type="Pancreas, pooled libraries Melton normalized mixed mouse pancreas 1 N1-MMS1, Amplified Melton mou se islets 1 M1S1-A, and Kaestner ngn3 wt." /clone_lib="NIH_MGC_137" /lab_host="DH10B" /note="vector: pSPORT1"
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Best Local Similarity:	92.7% Mismatches: 8

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Qy	41	GlnPheHisVallySerGlyLeuGlnLeuLysAsnAlaLeuLeuLeuLeuLeu	60
Db	2472	CAGTTCACGCTCAAGTCGGGCTTCAGATCGAAGAACGCCATCACCAGCAGTAC	2413
Qy	61	ValThrSerGlnValLeuGlyLeuGlyLeuLeuLeuLeuLeuLeuLeuLeu	80
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Qy	81	ArgThrGlnGlyLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaArg	100
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Qy	101	ValGluLeuHisTrpArgAlaSerGlnCysProHisLeuValArgLeuVal	120
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Qy	141	GluLeuPheSerArgLeuGlnAspArgGlyAspGlnAlaPheThrGluArg	160
Db	2172	GAGCTCTTTAGTCCAATCCAGGACCGAGGAGCAGGATTCACAGAAAGAGG	2113
Qy	161	GluLeuMetLysSerLeuGlyGluAlaLeuGlnTrpLeuHisSerLeuAla	180
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Qy	201	LeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThr	220
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Qy	221	TyrThrProTrpTyrValAlaProGluValLeuGlyProGluLysTyrAsp	240
Db	1932	TATACACCATACTATGTGGCTCGGAGTCTTGGGCGCGGAGAGTATGACAG	1873
Qy	241	AspMetTrpSerLeuGlyValLeuMetTyrIleLeuLeuCysGlyTyrPro	260
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Qy	301	LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsn	320
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361 ValAspTyrGluGlnLeuLysLysLysLysLeuAspAlaSerAsnProLeuLeuLeu 380  
 1048 GTTGACTATGACGATCAAGATAAAGATAGAGAGCGCATCAACCCCTCTGCTCTC 1107

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 1108 AAGAGCGGAGAAAGCTCGTGTGGAGGATCGGCTCTCGCCAC 1155

RESULT 13  
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 LOCUS  
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 ACCESSION AY335730  
 VERSION AY335730.1 GI:33304098  
 KEYWORDS FLI CDNA.  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.  
 REFERENCE 1 (bases 1 to 1065)  
 AUTHORS Park,J., Rolfs,A., Hu,Y., Murthy,T.V.S., Vannberg,F., Shen,B., Rolfs,A., Hutti,J.E., Cantley,L.C., Labaer,J., Harlow,E. and Brizuela,L.  
 TITLE Building a human kinase gene repository: Bioinformatics, molecular cloning, and functional validation  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 102 (23), 8114-8119 (2005)  
 PUBMED 15928075  
 REFERENCE 2 (bases 1 to 1065)  
 AUTHORS Park,J., Rolfs,A., Hu,Y., Shen,B., Vannberg,F., Moreira,D., Kelley,T., Zuo,D., Raphael,J., Baqui,M., Jepson,D., Harlow,E., Labaer,J. and Brizuela,L.  
 TITLE Direct Submission  
 JOURNAL Submitted (02-JUL-2003) Biological Chemistry and Molecular Pharmacology, Harvard Institute of Proteomics, 320 Charles St., Cambridge, MA 02141-2023, USA  
 COMMENT This CDS clone is a part of a collection of human full-length expression clones generated by Harvard Institute of Proteomics. Each CDS has been cloned without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In-Fusion(TM) cloning system between the SalI and HindIII sites of the pDNR-Dual vector. Additional sequences in the clone: 'ACC' after SalI site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindIII site to maintain reading frame.  
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## ORIGIN

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 Query Match: 83.8% Indels: 16  
 DB: 8 Gaps: 1

US-10-469-221-2 (1-396) x AY335730 (1-1065)

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 Db 67 -----CCCCCGCAGCAGTTCCCG 84  
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 Qy 61 ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnLysPheAsnLys 80  
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DEFINITION Methods and Compositions for Protein Expression and Purification.			
ACCESSION DD182194			
VERSION DD182194.1 GI:83957055			
KEYWORDS JP 2005514025-A/15.			
SOURCE synthetic construct			
ORGANISM other sequences: artificial sequences.			
REFERENCE 1 (Bases 1 to 1305) Tran,H.T., Malakhov,M.P. and Weeks,S.D.			
AUTHORS Malakhova,O.A., Butt,T.R.,			
TITLE Methods and Compositions for Protein Expression and Purification			
JOURNAL Patent: JP 2005514025-A 15 19-MAY-2005;			
Tauseef Butt, Stephen Weeks, Hiep Tran, Oxana Malakhova, Micheal			
Malakhov,			
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PD 19-MAY-2005			
PF 07-JAN-2003 JP 2003557532			
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malakhov,			
PI stephen d weeks			
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RESULT 15			
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ACCESSION CS214061			
VERSION CS214061.1 GI:83681911			
KEYWORDS Cricetulus longicaudatus (long-tailed hamster)			
SOURCE Cricetulus longicaudatus			
ORGANISM Cricetulus longicaudatus			
REFERENCE 1 Melville,M.W.			
AUTHORS Oligonucleotide arrays to monitor gene expression and methods for			
TITLE making and using same			
JOURNAL Patent: WO 2005111246-A 3380 24-NOV-2005;			
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## ORIGIN

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DB: 2 Gaps: 0

US-10-469-221-2 (1-396) x CS2114061 (1-1168)

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Db 841 GTCAAGGAGGAGATGACCAAGTGGCTTGGCCACGATGCGTGTGACTATGACGACATCAAG 900
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Qy 368 IleLysLysIleGluAspAlaSerAsnProLeuLeuLysArgGlyLysAlaArg 387  
Db 901 ATAAAGAAGATAGAAGACCGCATCCACCCCTCTGCTTCTGAAGAGCGGAAAGAGCTCGT 960

Qy 388 AlaLeuGluAlaAlaAlaLeuAlaHis 396

Db 961 GCCGTGGAGGCCGCGAGCCCTTGGCCAC 987

Search completed: June 19, 2006, 16:48:42  
Job time : 7503 secs

*This Page Blank (uspto)*

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 19, 2006, 15:07:48 ; Search time 6132 Seconds  
(without alignments)  
5416.843 Million cell updates/sec

Title: US-10-469-221-2

Perfect score: 2106

Sequence: 1 SQGSPVPFPAPAPPQP.....PLLLKRRKARALEMAAAAH 396

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 48236798 seqs, 2795965780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlh  
-Q=/abes/ABSWEB\_spool/US10469221/runat\_19062006\_062554\_1128/app\_query.fasta\_1  
-DB=EST -QPMT=fastcap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs04  
-USER=US10469221 @CGN\_1\_1\_6323 @runat\_19062006\_062554\_1128 -NCPU=6 -ICPU=3  
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est3:\*  
3: gb\_est4:\*  
4: gb\_est5:\*  
5: gb\_est6:\*  
6: gb\_btc:\*  
7: gb\_est2:\*  
8: gb\_est7:\*  
9: gb\_est8:\*  
10: gb\_est9:\*  
11: gb\_gss1:\*  
12: gb\_gss2:\*  
13: gb\_gss3:\*  
14: gb\_gss4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1931	91.7	2674	6	AK155171 Mus muscu
2	1577	74.9	901	8	CR980921 CR980921
3	1550	73.6	941	3	BQ884713 AGNCOURT
4	1500	71.2	850	9	DN107605 DN107605

5	1398	66.4	780	14	AY410229
6	1396	66.3	1182	9	DN666480 CFW32-D05
7	1393	66.1	780	14	AY410231 Mus muscu
8	1393	66.1	920	10	DT404291 JGI_CAB16
9	1391	66.0	1149	14	AY403347 Homo sapi
10	1391	66.0	1799	6	CR06251 full-leng
11	1384	65.7	3003	6	BC068497 Homo sapi
12	1361	64.6	1155	14	AY403349 Mus muscu
13	1361	64.6	2481	6	AK087496 Mus muscu
14	1361	64.6	2724	6	AK172344 Mus muscu
15	1361	64.6	2732	6	AK151881 Mus muscu
16	1359	64.5	842	5	CF617043 AGNCOURT
17	1347	64.0	2747	6	AK144637 Mus muscu
18	1344	63.8	902	10	DV928789 LB03014.C
19	1338	63.5	776	3	BU609266 UI-M-FR0-
20	1338	63.5	998	10	DW625395 CLJ345-C1
21	1337	63.5	2812	6	AK170456 Mus muscu
22	1328	63.1	883	8	CR440918 CR440918
23	1319.5	62.7	785	2	BG397545 602439376
24	1310	62.2	833	3	BU296673 603611177
25	1289	61.2	775	10	DT446795 JGI_CABK7
26	1287	61.1	728	5	CF725542 UI-M-GZ0-
27	1286	61.1	751	4	CB169658 RUC603000
28	1284	61.0	803	5	CF725030 UI-M-GZ0-
29	1283.5	60.9	875	5	CF582482 AGNCOURT
30	1272	60.4	795	8	CN224489 WLA056H05
31	1267	60.2	726	8	CN431763 170006001
32	1264	60.0	827	9	DN284271 1184539 M
33	1262	59.9	710	10	DR423458 nav26d01.
34	1256	59.6	764	2	B1150810 602914708
35	1255.5	59.6	784	8	CV102706 AGNCOURT
36	1238	58.8	756	8	CV804995 AGNCOURT
37	1236	58.7	742	3	BU424082 603231147
38	1233	58.5	739	2	BI077614 602871715
39	1228	58.3	720	2	BG779875 602667370
40	1224.5	58.1	727	8	CV783919 UI-M-HY0p
41	1224	58.1	732	3	BU314388 603542691
42	1212	57.5	729	9	DN933930 AGNCOURT
43	1209	57.4	690	10	DY113286 000311BSP
44	1208	57.4	690	7	AW918725 EST350029
45	1201	57.0	752	8	CK974173 4104800 B

#### ALIGNMENTS

RESULT 1	AK155171	2674 bp	mRNA	linear	HTC 21-SEP-2005
LOCUS	AK155171	Mus musculus NOD-derived CD11c +ve dendritic cells cDNA, RIKEN			
DEFINITION		full-length enriched library, clone: F630205L24 product: MAP			
		kinase-activated protein kinase 2, full insert sequence.			
ACCESSION	AK155171	GI:74199084			
VERSION	AK155171.1	HTC; CAP trapper.			
KEYWORDS		Mus musculus (house mouse)			
SOURCE		Mus musculus			
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.			
REFERENCE		1			
AUTHORS		Carninci, P. and Hayashizaki, Y.			
TITLE		High-efficiency full-length cDNA cloning			
JOURNAL		Meth. Enzymol. 303, 19-44 (1999)			
PUBLISHED		10349636			
REFERENCE		2			
AUTHORS		Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.			
TITLE		Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes			
JOURNAL		Genome Res. 10 (10), 1617-1630 (2000)			
PUBLISHED		11042159			
REFERENCE		3			
AUTHORS		Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,			







Heubnerweg 6, D-14059 Berlin, Germany  
Tel: +49 30 32639 100  
Fax: +49 30 32639 111  
[www.rzpd.de](http://www.rzpd.de)

This clone is available from RZPD;  
<http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=R2Pdp9016G1344>  
 contact RZPD (product- support@rzpd.de) for more information.  
 Primer name: a33 4 . Primer sequence: CGGTAACCAATTTCACACAG.

## FEATURES

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1. 901
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="RZPDp9016G1344"
/tissue_type="T-Lymphocytes"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="RZPD no.9016"
/note=vector: pQE80LSN_cloned; Site_1: SalI; Site_2:
NotI; vector:
http://www.rzpd.de/info/vectors/pQE80LSN_cloned_pic.shtml
; 1st strand cDNA was prepared from mRNA obtained from
human T-Lymphocytes with a NotI - oligo(dT) primer [5'
GACTAGTCATGATCGAGCGGCCGCCCTTTTTTTTTT 3'].
Double-stranded cDNA was ligated to SalI adaptors,
digested with NotI and cloned into the NotI and SalI sites
of the pQE80LSN cloned vector"

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## ORIGIN

Alignment Scores:		
Pred. No.:	1,978-125	301
Score:	1577.00	297
Percent Similarity:	99.0%	Conservative: 0
Best Local Similarity:	99.0%	Mismatches: 3
Query Match:	74.9%	Indels: 0
DB:	8	Gaps: 0

US-10-469-221-2 (1-396) x CR980921 (1-901)

Qy	55	Ile	Asp	Asp	Tyr	Ile	Val	Thr	Ser	Gln	Val	Leu	Gly	Ile	Asn	Gly	Val	74														
Db	1	AT	CA	TG	CA	TG	CA	TG	CA	TG	CA	TG	CA	TG	CA	TG	CA	60														
Qy	75	Leu	Gln	Ile	Phe	Asn	Lys	Arg	Thr	Gln	Glu	Lys	Phe	Ala	Leu	Lys	Met	Leu	Gln	Asp	Cys	94										
Db	61	TT	GC	CA	GA	TC	TT	CA	CA	AG	GA	GC	CC	CA	GA	GA	AA	TT	GC	CC	CT	CA	AA	AT	GC	TT	CA	GG	AC	TG	CG	120
Qy	95	Pro	Lys	Ala	Arg	Arg	Glu	Val	Glu	Leu	His	Str	Arg	Ala	Ser	Gln	Cys	Pro	His	Ile	Val	114										
Db	121	CCC	AAG	CCC	CGG	CAGG	GAG	GGT	GAG	CTG	CACT	TGG	CGG	GCT	CCC	CAG	TGC	CGG	CGC	CA	TCG	TA	180									
Qy	115	Arg	Ile	Val	Asp	Val	Tyr	Glu	Asn	Leu	Tyr	Ala	Gly	Arg	Lys	Cys	Lys	Leu	Leu	Ile	Val	Met	134									
Db	181	CGG	AT	CGT	CGT	AT	CTG	TAC	GAGA	AT	CTG	TAC	GAG	GAG	AA	GTG	CGT	CTG	CTG	TA	TGT	CA	TG	240								
Qy	135	Glu	Cys	Leu	Asp	Gly	Gly	Leu	Phe	Ser	Arg	Ile	Gln	Asp	Arg	Gly	Asp	Gln	Ala	Phe	154											
Db	241	GAA	TG	TT	CG	AC	GGT	GG	AGA	CT	TTT	TAC	CG	AA	TCC	AGG	AT	CG	AG	GAG	ACC	AG	CA	TC	300							
Qy	155	Thr	Glu	Arg	Glu	Ala	Ser	Glu	Ile	Met	Lys	Ser	Ile	Gly	Glu	Ala	Ile	Gln	Tyr	Leu	His	174										
Db	301	AC	AGA	AA	GAG	AG	CA	TC	CC	GA	AT	CA	TAG	AG	CA	TC	CGT	GAG	GCC	AT	CC	AG	TAT	CG	360							
Qy	175	Ser	Ile	Asn	Ile	Ala	His	Arg	Asp	Val	Lys	Pro	Glu	Asn	Leu	Tyr	Thr	Ser	Lys	Arg	194											
Db	361	TCA	AT	CA	AA	TG	CC	CA	TG	CGG	AT	GT	CA	AG	CC	TG	AGA	AT	CT	CT	TAT	AC	CT	CC	CA	AA	AG	420				
Qy	195	Pro	Asn	Ala	Ile	Leu	Lys	Leu	Thr	Asp	Phe	Gly	Phe	Ala	Lys	Glu	Thr	Thr	Ser	His	Asn	214										
Db	421	CCC	AA	CG	CC	AT	CT	CG	AA	AT	CT	CA	CT	GAC	TTT	TG	CG	CTT	TG	CA	AG	GA	AA	CC	CA	CG	CC	CA	AC	480		
Qy	215	Ser	Leu	Thr	Thr	Pro	Cys	Tyr	Thr	Pro	Tyr	Val	Ala	Pro	Glu	Val	Leu	Gly	Pro	Glu	234											

Db	481	TC	TTTGACCACTCCTTGTATATACACCGTACTATGTGGCTCCAGAGTGTGGGTCCAGAG	540
Qy	235	Lys	TyrAspLysSerCysAspMetTrrPsrLeuGlyValIleMetTyrIleLeuLeuCys	254
Db	541	AAG	TATGACAAAGTCCTGTGACATGTGGTCCCTGGGTGCATCATGTATCATCTCGCTGTGT	600
Qy	255	Gly	TyrProPheTyrSerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArg	274
Db	601	GGG	TATCCCCCTTCTACTCAACACGGCTTGGCCATCTCTCCGGCATGAAGATCGC	660
Qy	275	Ile	ArgMetGlyGlnTyrGluPheProAsnProGluTrrPsrGluValserGluGluVal	294
Db	661	AT	CGAATGGCGCAGTATGAATTTCCCAACCCAGAATGGTCAGAAATATCAGAGGAATG	720
Qy	295	Lys	MetLeuIleArgAsnLeuLysThrGluProThrGlnArgMetThrIleThrGlu	314
Db	721	AAG	ATGCTCATTCGGAAATCTGCTAAACAGAGCCCAACCCAGAGANTGACCATCCTAG	780
Qy	315	Phe	MetAsnHisProTrrIleMetGlnSerThrLysValProGlnThrProLeuHisThr	334
Db	781	TTT	ATGAACACCTTGGATCATGCAATCAACAAGGTCCCTCAACCCCACTGCACACC	840
Qy	335	Set	ArgValLeuLysGluAspLysGluArgTrrPgluAspValLysGluMetThrSer	354
Db	841	AGC	CGGTCTGAANGAGGCAAGAGGCGGTGGGANGATGCTAAGGAGGAATGACCACT	900

RESULT 3

BQ884713

LOCUS

DEFINITION  
 AGENCOURT\_8747447 NIH\_MGC\_130 Mus musculus cDNA clone IMAGE:6336305  
 5', mRNA sequence.

ACCESSION

BQ884713

VERSION

BQ884713.1

GI:22276731

KEYWORDS

EST.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroides; Muridae; Murinae; Mus.  
 NIH-MGC <http://mgi.nci.nih.gov/>.  
 1 (bases 1 to 941)

AUTHORS

National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE

Unpublished (1999)

JOURNAL

Contact: Robert Strausberg, Ph.D.

COMMENT

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
 Tissue Procurement: Mark Maconochie, Ph.D. and Nancy L. Freeman, Ph.D.  
 cDNA Library Preparation: ResGen, Invitrogen Corp  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLAM13800 row: b column: 18  
 High quality sequence stop: 700.

FEATURES

source

1. 941  
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 /mol\_type="mRNA"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:6336305"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_130"  
 /note="Organ: oocytes; Vector: pCMV-SPORT6.1; Site: 1: EcoRV; Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.95 kb. Constructed by ResGen, Invitrogen Corp. Note: this is a NIH\_MGC Library."

ORIGIN

Alignment Scores:  
 Pred. No.: 4.43e-123 Length: 941  
 Score: 1550.00 Matches: 302  
 Percent Similarity: 97.5% Conservative: 4

Best Local Similarity: 96.2%		Mismatches: 4	
Query Match: 73.6%		Indels: 4	
DB: 3		Gaps: 0	
US-10-469-221-2 (1-396) x BQ884713 (1-941)			
Qy	76	GlnIlePheAsnLysArgThrGlnGluLysPheAlaLeuLysMetLeuGlnAspCysPro	95
Db	2	CGGATCTTCACAGAGAACCCAGCAAAATTCGCCCTAAAGATGCTCCAGGACTGTCG	61
Qy	96	LysAlaArgGluValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArg	115
Db	62	AAGCGCGCAGAGAGGTGGAGTCACTCGAGGCCCTCCAGTGGCCACACATTTGTCAC	121
Qy	116	IleValAspValTyrGluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGlu	135
Db	122	ATCGTGATGCTATGAGAACCTGTATGCCGGAGGAGTGCCTGCTGATTTGTCATGGAG	181
Qy	136	CysLeuAspGlyGlyGluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThr	155
Db	182	TGTCCTCATGTCGAGAGCTCTTTAGTCGAATCCAGGACCGAGGAGCAGGCATTCACA	241
Qy	156	GluArgGluAlaSerGluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSer	175
Db	242	GAAGAGAGGCGTCAGAGATCATGAAGAGCATGCGGAGGCCATCCAGTACCTGCACCTCG	301
Qy	176	IleAsnIleAlaHisArgAspValLysProGluAsnLeuTyrThrSerLysArgPro	195
Db	302	ATCAACATTTGCTACCGGATGTCACCGTTCAGACCTCTATATATCTTCCAAAGGCC	361
Qy	196	AsnAlaIleLeuLysLeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSer	215
Db	362	AATGCCATTTTGAACACTCACTGATTTTGGCTTTGGCCAAAGAAACCCAGTCACAACTCT	421
Qy	216	LeuThrThrProCysTyrThrProTyrTyrValAlaProGluValLeuGlyProGluLys	235
Db	422	TTGACCACTCCGTGTTATACCACTACTATGTGGCTCCGGAAGTCTCGGCGCGGAGAG	481
Qy	236	TyrAspLysSerCysAspMetTrpSerLeuGlyValIleMetTyrIleLeuLysCysGly	255
Db	482	TATGACAAATGCTGTGACATGTGGTCTTGGGTGTCATCATGTATATTTGCTGTGGG	541
Qy	256	TyrProPheTyrSerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIle	275
Db	542	TATCCCCCTCTTATTCCAATCAGCGCTTGGCCATCTCTCCGGCATGAAGACTCGTATT	601
Qy	276	ArgMetGlyGlnTyrGluPheProAsnProGluTrpSerGluValSerGluGluValLys	295
Db	602	CGAATGGCGCAGTATGAATTTCTTAACCGGAGTGGTTCAGAAGTATCAGAAGAAGTGAAG	661
Qy	296	MetLeuIleArgAsnLeuLysThrGluProThrGlnArgMetThrIleThrGluPhe	315
Db	662	ATGCTTATCCGGAATCTGCTAATAACAGAGCCACCCAGAGATGACCATCACAGAATTC	721
Qy	316	MetAsnHisProTrpIleMetGlnSerThrLysValProGlnThrProLeuHisThrSer	335
Db	722	ATGAACCAACCCCTGGATGTCATCTACGAAGGTCCCTCAGACTCCACTGCACACAGC	781
Qy	336	ArgValLeuLysGluAspLysGluArg-TrpGluAspValLysGlu-GluMetThrSer	354
Db	782	CNFTGTCCTGAAGAGGACAAAGACCGATGGAGGATGTCAAAGGAGGAGATGACCACT	841
Qy	355	AlaLeu-AlaThrMetArgValAspTyrGluGlnIleLysIleLysIleGluAspAl	374
Db	842	GCCTTGGGCCACATGCTGTTGACTATGACGAGATCCAGATTAAGAAGATAGAGAGCG	901
Qy	374	aSerAsnProLeuLeuLysArgArgLysLys	385
Db	902	ATCAACCCCTCTGCTCTCAAGAGCGGGAAGAAG	935
RESULT 4			
DN107605			
LOCUS			
		850 bp	mRNA linear EST 14-FEB-2005

DEFINITION	110S067 MARC 4PIG Sus scrofa cDNA 5', mRNA sequence.		
ACCESSION	DN107605		
VERSION	DN107605.1		
KEYWORDS	EST.		
SOURCE	Sus scrofa (pig)		
ORGANISM	Sus scrofa		
REFERENCE	1 (bases 1 to 850)		
AUTHORS	Smith,T.P.L., Freking,B.A., Ford,J.J., Vallet,J.L., Wise,T.A., Noneman,D.J., Wray,J.E. and Reece,J.W.		
TITLE	Porcine EST collection using a normalized library constructed from embryos representing early developmental stages		
JOURNAL	Unpublished (2003)		
COMMENT	Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390 Email: smith@email.marc.usda.gov Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross_match v0.990329. Plate: HHY8003 row: B column: 15 Seq primer: GTAATACGACTCATATTAGG.		
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ORIGIN			
Alignment Scores:			
Pred. No.:	7..9e-119		
Score:	1500.00		
Percent Similarity:	100.0%		
Best Local Similarity:	99.3%		
Query Match:	71.2%		
DB:	9		
US-10-469-221-2 (1-396) x DN107605 (1-850)			
Qy	52	LysAsnAlaIleIleAspAspTyrLysValThrSerGlnValLeuGlyLeuGlyIleAsn	71
Db	2	AGAAGCGCATCATCGACGACTACAAGGTCAACCCAGGTCCTGGGACTGGGCATCAAC	61
Qy	72	GlyLysValLeuGlnIlePheAsnLysArgThrGlnGluLysPheAlaLeuLysMetLeu	91
Db	62	GGGAAAGTTTTTCAGATCTTCAACAAGAGGACCCAGGAGAAATTCGCCCTAAAAATGCTT	121
Qy	92	GlnAspCysProLysAlaArgGluValGluLeuHisTrpArgAlaSerGlnCysPro	111
Db	122	CAGGACTGTGCCAAGCCCGCGGAGGTGGAGTGCACCTGGCGGGCTCTCCAGTGGCCCA	181
Qy	112	HisIleValArgIleValAspValTyrGluAsnLeuTyrAlaGlyArgLysCysLeuLeu	131
Db	182	CACATCGTCGGATCGTGGACGCTCTATGAGAACCTGTACGCGGGGAGGAGTGCCTACTG	241
Qy	132	IleValMetGluCysLeuAspGlyGlyGluLeuPheSerArgIleGlnAspArgGlyAsp	151
Db	242	ATCGTCATGGAGTGTGGATGGTGGAGAACTCTTTAGCCGAATCCAGGACCGAGAGAG	301
Qy	152	GlnAlaPheThrGluArgGluAlaSerGluIleMetLysSerIleGlyGluAlaIleGln	171
Db	302	CAAGCGTTTCACAGAAAGAGGCGCATCAGAAATCATGAAGACATTTGGTAGGCCATCCAG	361

DEFINITION		1105067 MARC 4Pig Sus scrofa cDNA 5', mRNA sequence.	
ACCESSION		DN107605	
VERSION		DN107605.1	
KEYWORDS		GI:59782868	
SOURCE		EST.	
ORGANISM		Sus scrofa (pig)	
REFERENCE		Sus scrofa	
AUTHORS		Smith, I.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Wise, T.A., Nonneman, D.J., Wray, J.E. and Keele, J.W.	
TITLE		Porcine EST collection using a normalized library constructed from embryos representing early developmental stages	
JOURNAL		Unpublished (2003)	
COMMENT		Contact: Smith TPL	
		USDA, ARS, US Meat Animal Research Center	
		PO Box 166, Clay Center, NE 68933-0166, USA	
		Tel: 402 762 4366	
		Fax: 402 762 4390	
		Email: smith@email.marc.usda.gov	
		Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross_match v0.990329.	
		Plate: HHY8003 row: B column: 15	
		Seq primer: GTAATACGACTCACTATAGG.	
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		/db_xref="taxon:9823"	
		/tissue_type="pooled"	
		/lab_host="DH10B"	
		/clone_lib="MARC 4Pig"	
		/notes="Vector: pCDNA3.1; Site_1: EcoRI; Site_2: NotI; Library made with combined RNA from day-10, day-13, day-15, day-25, and day-30 whole embryos."	
ORIGIN			
Alignment Scores:			
Pred. No.:		7.9e-119	Length: 850
Score:		1500.00	Matches: 281
Percent Similarity:		100.0%	Conservative: 2
Best Local Similarity:		99.3%	Mismatches: 0
Query Match:		71.2%	Indels: 0
DB:		9	Gaps: 0
US-10-469-221-2 (1-396) x DN107605 (1-850)			
Qy	52	LysAsnAlaIleIleAspAspTyrLysValThrSerGlnValLeuGlyLeuGlyIleAsn	71
Db	2	AAGAACCCATCATCGACGACTACAGGTCAACCCAGGTCTGGAGTGGGCATCAAC	61
Qy	72	GlyLysValLeuGlnIlePheAsnLysArgThrGlnGluLysPheAlaLeuLysMetLeu	91
Db	62	GGGAAAGTTTTCAGATCTTCAACAGAGAGGCCAGGAGAAATTCGCCCTAAAAATGCTT	121
Qy	92	GlnAspCysProLysAlaArgGluValGluLeuHisTrpArgAlaSerGlnCysPro	111
Db	122	CAGGACTGTCCCAAGGCCCGCCGAGGTGGAGTGCCTCTGGCGGCCCTCCCGAGTCCCA	181
Qy	112	HisIleValArgIleValAspValTyrGluAsnLeuTyrAlaGlyArgLysCysLeuLeu	131
Db	182	CACATCGTCGGATCGTGGACGCTATGAGACCTGTACCGGGAGGAGTGCCTACTG	241
Qy	132	IleValMetGluCysLeuAspGlyGlyGluLeuPheSerArgIleGlnAspArgGlyAsp	151
Db	242	ATCGTCATGGAGTGTGGATGGTGGAGAACTTTTAGCCGAATCCAGGACCCAGGAGAC	301
Qy	152	GlnAlaPheThrGluArgGluAlaSerGluIleMetLysSerIleGlyGluAlaIleGln	171
Db	302	CAAGCGTTACAGAAAGAGAGGCGATCAGAAATCATGAAGAGCATTTGGTGGGCCATCCAG	361



VERSION	DN666480.1	GI:61986536	
KEYWORDS	EST.		
SOURCE	Gasterosteus aculeatus (three spined stickleback)		
ORGANISM	Gasterosteus aculeatus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes; Gasterosteidae; Gasterosteus.		
AUTHORS	1 (bases 1 to 1182) Kingsley, D.M., Peichel, C., Balabhadra, S., Grimwood, J., Dickson, M., Schmutz, J. and Myers, R.M.		
TITLE	Expressed sequence tags from Gasterosteus aculeatus		
JOURNAL	Unpublished (2003)		
COMMENT	Contact: Grimwood, Jane Stanford Human Genome Center Stanford University School of Medicine 975 S California Ave, Palo Alto, CA 94304, USA Tel: 650 320 5917 Fax: 650 320 5801 Email: jane@shgc.stanford.edu Plate: 32		
FEATURES	High quality sequence stop: 831.		
source	Location/Qualifiers		
	1..1182		
	/organism="Gasterosteus aculeatus"		
	/mol_type="mRNA"		
	/strain="Conner Creek sticklebacks, WA USA"		
	/db_xref="taxon:69293"		
	/clone="CPW32-D05"		
	/sex="mixed male and female"		
	/tissue_type="gills"		
	/dev_stage="adult"		
	/lab_host="DH10B (T1 phage resistant)"		
	/clone_lib="SHGC-CFW"		
	/note="Vector: Express 1; Total and poly A+ RNA was isolated from the indicated stickleback tissue, and a cDNA library was constructed in the Express 1 plasmid vector by Open Biosystems. First strand cDNA synthesis was primed with an 54 bp linker primer containing an oligodT sequence preceded by a synthetic NotI site (first strand primer: 5'-GACTAGTCTAGATCGCGCGGCC(T)25-3'). Following second strand synthesis, cDNAs were made blunt at the end corresponding to the original 5 prime end of mRNA, and cloned directionally into the NotI and EcoRV sites of Express 1. Note that the EcoRV site is typically destroyed in the blunt end cloning, leaving a junction of the form 'xxxATC' (where ATC is the second half of the EcoRV site, and xxx is derived from the cDNA sequence). A map of the Express 1 vector is available at: <a href="http://www.openbiosystems.com/cdna">http://www.openbiosystems.com/cdna</a> library construction fa q.php#8 The primary library was transformed and amplified in DH10B (T1 phage resistant) bacteria. Clones available from Open Biosystems: <a href="http://www.openbiosystems.com/stickleback">http://www.openbiosystems.com/stickleback</a> "		
ORIGIN			
Alignment Scores:			
Pred. No.:	1..12e-109	Length:	1182
Score:	1395.00	Matches:	262
Percent Similarity:	93.6%	Conservative:	18
Best Local Similarity:	87.6%	Mismatches:	18
Query Match:	66.3%	Indels:	1
DB:	9	Gaps:	0
US-10-469-221-2 (1-396) x DN666480 (1-1182)			
Qy	90	MetLeuGlnAspCysProLysAlaArgGluValGluLeuHisTrpArgAlaSerGln	109
Db	2	ATGCTGAGGATTGTGCCAAGCCCGTAGGAAAGTGGAGTGCACCTGGAGGGCTTCTCCC	61
Qy	110	CysProHisLeuValArgLeuValAspValTyrcGluAsnLeuTyrcAlaGlyArgLysCys	129
Db	62	TGTGCCAACATTGTGGCCATTCATTGATGTCTATGAGAACCTCTATCAGACGAGAGTGT	121
Qy	130	LeuLeuIleValMetGluCysLeuAspGlyGlyGluLeuPheSerArgIleGlnAspArg	149
Db	122	CTGCTATTTCATGGAGTCATGATGGTGGTGGAGCTTTTAGTCGAATCCAGCAGACA	181
Qy	150	GlyAspGlnAlaPheThrGluArgGluAlaSerGluIleMetLysSerIleGlyGluAla	169
Db	182	GGAGATCAGGCTTTTCACAGAGCGAGAGCGCTCTGACATCATCAAAACATCGGCGAGCC	241
Qy	170	IleGlnTyrcLeuHisSerIleAsnIleAlaHisArgAspValLysProGluAsnLeuLeu	189
Db	242	ATTTCAGTTCCTGATGCCGTCACATTTGCTCACAGACGTCACAGCAGAACTTACTG	301
Qy	190	TyrThrSerLysArgProAsnAlaIleLeuLysLeuThrAspPheGlyPheAlaLysGlu	209
Db	302	TATTCTCAAAGAGGCCCAACGCCCTCTCAAACTCACAGATTTTGGCTTTGCCAAGGAA	361
Qy	210	ThrThrSerHisAsnSerLeuThrThrProCysTyrcThrProTyrcValAlaProGlu	229
Db	362	ACCACCTCCCAACAACCTTTTAGCTACTCCGTGCTACACCCCTACTATGTGTCCAGAA	421
Qy	230	ValLeuGlyProGluLysTyrcAspLysSerCysAspMetTrpSerLeuGlyValIleMet	249
Db	422	GTTCCTGGCCACAGAAATATGACAGTCATGTGACATGTGTCACCTGGTGTCTATG	481
Qy	250	TyrIleLeuLeuCysGlyTyrcProPheTyrcSerAsnHisGlyLeuAlaIleSerPro	269
Db	482	TATATCTCTGTGTGGATACCTCTCTTTTATTCAAACACCGTTTAGCCATCTCTCT	541
Qy	270	GlyMetLysThrArgIleArgMetGlyGlnTyrcGluPheProAsnProGluTrpSerGlu	289
Db	542	GGGATGAAGAAGAGGATCAGATGGGCCAATATGAGTTTCCAAACCCCTGAGTGTCTGAC	601
Qy	290	ValSerGluGluValLysMetLeuIleArgAsnLeuLysThrGluProThrGlnArg	309
Db	602	GTATCAGAGGAGCAAAACAACTGATTAGGACTCTCTTAAGACTGAGCCCAACCCAGG	661
Qy	310	MetThrIleThrGluPheMetAsnHisProTrpIleMetGlnSerThrLysValProGln	329
Db	662	ATGACCATCACCGAATTCATGATTAATCCCTGGATCAATCAATCGATGGAGGTCTCC	721
Qy	330	ThrProLeuHisThrSerArgValLeuLysGluAspLysGluArgTrpGluAspValLys	349
Db	722	ACCCCACTTCACACCGCGGGTGTAAAGGAGGAGGAGCGCGTGNAGGAGTGTCAAG	781
Qy	350	GluGluMetThrSerAlaLeuAlaThrMetArgValAspTyrcGluGlnIleLysIleLys	369
Db	782	GAGAAATGACCAAGTGCCTTGGNCAATGAGAGTGCATACGAGCAAAATNCAGATCAAG	841
Qy	370	LysIleGluAspAlaSer-AsnProLeuLeuLysArgArgLysLysAlaArg	387
Db	842	ACCATGAGGACTCGACCCCAATCCCTGCTTAACAAAAAGAAAGAAAGACCCGT	896
RESULT 7			
AY410231		780 bp	DNA linear
LOCUS			GSS 16-DEC-2003
DEFINITION	Mus musculus MAPKAPK2 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.		
ACCESSION	AY410231		
VERSION	AY410231.1	GI:39766199	
KEYWORDS	GSS.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	1 (bases 1 to 780) Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B., Perrier, S., Wang, G., Zheng, X.H., White, T.J., Smirsky, J.J., Adams, M.D. and Cargill, M.		
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios		

```

JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 780)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Clivello,D.R., Lu,F., Murphy,B.,
Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
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/gene="MAPKAPK2"
/locus_tag="HCM3821"
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Alignment Scores:
Pred. No.: 1.18e-109 Length: 780
Score: 1393.00 Matches: 259
Percent Similarity: 99.6% Conservative: 0
Best Local Similarity: 99.6% Mismatches: 1
Query Match: 66.1% Indels: 0
DB: 14 Gaps: 0
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Qy 90 MetLeuGlnAspCysProLysAlaArgGluValGluLeuHisTrpArgAlaSerGln 109
Db 1 ATGCTCCAGGACTGTCGAAAGCGCGCAGAGAGTGAGCTGCACCTGGAGGGCTCCACG 60
Qy 110 CysProHisLeValArgIleValAspValTyrGluAsnLeuTyrAlaGlyArgLysCys 129
Db 61 TGCCACACATGTGACATCGTGGATGCTATGAGAACCTGTATGCCGGGAGGAAGTGC 120
Qy 130 LeuLeuIleValMetGluCysLeuAspGlyGlyGluLeuPheSerArgIleGlnAspArg 149
Db 121 CTGCTGATTGCTGGAGTGTCTGATGGTGGAGAGCTCTTAGTCGAATCCAGGACCGA 180
Qy 150 GlyAspGlnAlaPheThrGluArgGluAlaSerGluIleMetLysSerIleGlyGluAla 169
Db 181 GGAGACGAGGCATTACAGAAAGAGAGAGCGTCAGAGATCATGAGAGCATCGCGAGGCC 240
Qy 170 IleGlnTyrLeuHisSerIleAsnIleAlaHisArgAspValLysProGluAsnLeuLeu 189
Db 241 ATCCAGTACCTGCACTCGATCAACATTTGCTACCGGGATGTCAAGCTTGAGACCTCTTA 300
Qy 190 TyrThrSerLysArgProAsnAlaIleLeuLysLeuThrAspPheGlyPheAlaLysGlu 209
Db 301 TATACTTCCAAAGGCCCAATGCCATTTTGAAACTACTGATTTTGGCTTTGCCAAGGAA 360
Qy 210 ThrThrSerHisAsnSerLeuThrThrProCysTyrThrProTyrTyrValAlaProGlu 229
Db 361 ACCACCACTCACACTCTTTGACCACCTCCGTTGTATACACCATCATATGTGGTCCGGAA 420
Qy 230 ValLeuGlyProGluLysTyrAspLysSerCysAspMetTrpSerLeuGlyValIleMet 249
Db 421 GTCTCGGGCCGGAGAGATGACAAAGTCTGTGACATGTGGTCTTGGTGGTGTCAATCATG 480
Qy 250 TyrIleLeuLeuCysGlyTyrProProPheTyrSerAsnHisGlyLeuAlaIleSerPro 269
Db 481 TATATTTTGTGTGGGTATCCCCCTTCTATTCCAAATCACGGCTTGCCTCTCTCCG 540
Qy 270 GlyMetLysThrArgIleArgMetGlyGlaTyrGluPheProAsnProGluTrpSerGlu 289
Db 541 GCGATGAAGACTCGTATTCGAATGGCCAGTATGAATTTCTTAACCCGGAGTGTGCAGAA 600
Qy 290 ValSerGluGluValLysMetLeuIleArgAsnLeuLeuLysThrGluProThrGlnArg 309

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Db 601 GTATCAGAAAGTGAAGATGCTTATCCGGAATCTCTTAAAAACAGAGCCACCCAGAGA 660
Qy 310 MetThrIleThrGluPheMetAsnHisProTrpPileMetGlnSerThrLysValProGln 329
Db 661 ATGACCATCACAGAAATTCATGAACACCCCTCGATCATGCAATCTACGAAGGTCCCTCAG 720
Qy 330 ThrProLeuHisThrSerArgValLeuLysGluAspLysGluArgTrpGluAspValLys 349
Db 721 ACTCCACTGCACACCGCCGTGCTTGAAGAGGACGAAGGACGATGGGAGGATGTCAAG 780
RESULT 8
LOCUS DT404291 920 bp mRNA linear EST 25-AUG-2005
DEFINITION JGI_CABI6679.fwd NIH_XGC tropOv11 Xenopus tropicalis cDNA clone
IMAGE:7859151 5', mRNA sequence.
ACCESSION DT404291
VERSION DT404291.1 GI:73790488
KEYWORDS EST.
SOURCE Xenopus tropicalis (western clawed frog)
ORGANISM Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Xenopus; Silurana.
REFERENCE 1 (bases 1 to 920)
AUTHORS Richardson,P., Lucas,S., Rokhsar,D., Detter,J.C., Ng,D.C.,
Brockstein,P. and Lindquist,E.A.
TITLE DOE Joint Genome Institute Xenopus tropicalis EST project
JOURNAL Unpublished (2004)
COMMENT Other ESTs: JGI_CABI6679.rev
Contact: Lindquist,E.A., Richardson,P.
DOE Joint Genome Institute
2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Tel: 925 296 5600
Fax: 925 296 5710
Email: cdna@jgi-psf.org
Tissue Procurement: Robert M. Grainger
CDNA Library Preparation: Bruce Blumberg Laboratory, University of
California, Irvine
CDNA Library Arrayed by: DOE Joint Genome Institute:
http://www.jgi.doe.gov
DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
Clone Distribution: I.M.A.G.E. Consortium/LLNL:
http://image.llnl.gov
Naming Conventions: EST name is generated by the concatenation of
the JGI Clone id and the direction of sequencing. The suffix '.fwd'
indicates a forward sequencing read of the insert. It does not
necessarily reflect the orientation of the insert.
Plate: CABI 0069 row: n column: 13
High quality sequence stop: 783.
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/dev_stage="Adult"
/lab_host="ElectroMAX DH10B T1 Phage Resistant cells"
/clone_lib="NIH_XGC tropOv11"
/notes="Vector: pCSI07; Site_1: EcoRI; Site_2: XhoI; The
library was prepared from 5 ug of poly A+ RNA by oligo-dT
priming
(5'-ACTAGTCGGCGCTAGCCTCGAGTTTCTTTTCTTTTCTTTT-3') and
Stratascript reverse transcriptase. After ligation of
EcoRI adapters (5'-AATTCGGCAGCAGG-3') followed by kinasing
adapters and by XhoI digestion, the cDNA was size selected
by chromatography on Sepharose CL-2B columns and fractions
containing cDNAs larger than 1000 bp were ligated into
EcoRI/XhoI-digested pCSI07. Reference for library
construction: Current Genomics 4, 635-644. Library

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constructed by Michelle Tabb and Bruce Blumberg (Dept of Developmental and Cell Biology, University of California, Irvine)."

## ORIGIN

Alignment Scores:  
 Pred. No.: 1.46e-109 Length: 920  
 Score: 1393.00 Matches: 265  
 Percent Similarity: 93.0% Conservative: 16  
 Best Local Similarity: 87.7% Mismatches: 21  
 Query Match: 66.1% Indels: 1  
 DB: 10 Gaps: 0

US-10-469-221-2 (1-396) x DT404291 (1-920)

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Qy 37 GlnGlnPheProGlnPheHisValLysSerGlyLeuGlnIleLysLysAsnAlaIle 56
Db 14 CAACAACACAGCAGCAGCAACTTAAGTCTACTTTCAAATATAAAGAAATGCCATAACT 73
Qy 57 AspAspTyrLysValThrSerGlnValLeuGlyLeuGlyLysAsnGlyLysValLeuGln 76
Db 74 GATGACTACAAGTCACTAATCAGGTCTTGAGACTGGGATCAACGGGAAGGTGCTAGAG 133
Qy 77 IlePheAsnLysArgThrGlnGlnLysPheAlaLeuLysMetLeuGlnAspCysProLys 96
Db 134 ATCTTCAGTAAGAAGTCTGGAGAGAAGTTCGCTATGAAGATGTTACAGGACTGTGCAAG 193
Qy 97 AlaArgGluValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIle 116
Db 194 GCACGCGAGGAGGTAGAACTGCTACCTGGCGGCTTCCAGAGTGTTCATATCGTGAAGATT 253
Qy 117 ValAspValTyrGluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCys 136
Db 254 ATTGATGTGTACGAAATCTATACAGTCTAGAAGTGTCTCTATTATTATGGAATGT 313
Qy 137 LeuAspGlyGlyGluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGlu 156
Db 314 CTGGATGAGGAGCAACTCTTCAGCAGAAATCCAGATAGAGGGGACCAAGCTTTCACGGAG 373
Qy 157 ArgGluAlaSerGluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIle 176
Db 374 AGGGAGGCACTGATGATCATGAGAAAGCAATTCGAGAAGCAATTCAGTACTTACACTCTATC 433
Qy 177 AsnIleAlaHisArgAspValLysProGluAsnLeuLeuTyrThrSerLysArgProAsn 196
Db 434 AATATTGCCATAGAGATGTAAGCCAGAAATCTCTATATACATCGAAACGCCCAAC 493
Qy 197 AlaIleLeuLysLeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeu 216
Db 494 TCAGTGTAAAGCTGACTGATTTTGGTTTCTAAGGAAACCAATCACACAAATTCACATA 553
Qy 217 ThrThrProCysTyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyr 236
Db 554 GCAACACCTTGTACACACCTTATTATGTTCTCTCTGAAAGTCTCGGGCCAGAAAAATAT 613
Qy 237 AspLysSerCysAspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyr 256
Db 614 GACAAGTCGTGTATATGTGTCTCTAGGTGTATCATGTACATTCTACTATGTGGCTAT 673
Qy 257 ProProPheTyrSerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArg 276
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Qy 277 MetGlyGlnTyrGluPheProAsnProGluTrpSerGluValSerGluGluValLysMet 296
Db 734 ATGGGCCAGTATGAATTTCCAAACCCAGAGTGGTCTGAAGTTCAGATGAAGTANAACAG 793
Qy 297 LeuIleArgAsnLeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMet 316
Db 794 TTGATCAGAAATCTTTTGAAGACTGAGCCAACTCAGAGGATGACATCACAGAAATTTATG 853
Qy 317 AsnHisProTrpIleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArg 336
  
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Db 854 AACCATCTTTGGATACGCAGCTCTATGCAGATTCCACC-ACACCTCTTCATACAGCAGG 912
Qy 337 ValLeu 338
Db 913 GTCTTG 918

RESULT 9
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LOCUS Homo sapiens MAPKAPK3 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION Genomic survey sequence.
ACCESSION AY403347
VERSION AY403347.1 GI:39759330
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 1149)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1149)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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ORIGIN
Alignment Scores:
Pred. No.: 2.92e-109 Length: 1149
Score: 1391.00 Matches: 265
Percent Similarity: 80.2% Conservative: 50
Best Local Similarity: 67.4% Mismatches: 56
Query Match: 66.0% Indels: 22
DB: 14 Gaps: 3

US-10-469-221-2 (1-396) x AY403347 (1-1149)
Qy 1 SerGlnGlyGlnSerProValProPheProAlaProAlaProProGlnProPro 20
Db 16 GCAGAGGAGCAGGGGGGCCCTGTGCC- - - - -CGGCCAGTTGCACCCGCG 60
Qy 21 ThrProAlaLeuProHisProAlaGlnProProProProGlnGlnPhePro 40
Db 61 GGACCCCGGCTTGGCGGTGCTCCGGGGGGCGGGAGGCC- - - - - 102
Qy 41 GlnPheHisValLysSerGlyLeuGlnIleLysLysAsnAlaIleLeuAspTyrLys 60
Db 103 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - 132
Qy 61 ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLys 80
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Qy 81 ArgThrGlnGluLysPheAlaLeuLysMetIeuGlnAspCysProLysAlaAaArgGlu 100
Db 193 CGCACTGAGACAGTGTGGCTTCTGATGACAGAGCCCAAGAGGCGGCGAGGAG 252
Qy 101 ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr 120
Db 253 GTAGACCATCAGTGGCAGGCTTGGCGGCCCCCATATTGTCGATCTCCGATGGATGTAT 312
Qy 121 GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly 140
Db 313 GAGAACATGCACCATGCAAGCGTGTCTCTCATCATCATGGAATGCATGGAAGGTGT 372
Qy 141 GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer 160
Db 373 GAGTTGTTTCAGCAGGATTCAGGAGCGTGGCGACGAGCTTTCATCTGAGAGAGAGCTGCA 432
Qy 161 GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis 180
Db 433 GAGATAATGGGATATTGGCACTGCCATCAGTTCTTGACAGCCCATACATATGCCAC 492
Qy 181 ArgAspValLysProGluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeuLys 200
Db 493 CGAGATGTCAGGCTGAAACCTACTCTACACATCTAAGGAGAAAGACGAGTCTTAAG 552
Qy 201 LeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCys 220
Db 553 CTCACCATTTTGGCTTGTGAAGGAGACCAACC---CAAAATGCCCTGCACACCCCTGC 609
Qy 221 TyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys 240
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Qy 241 AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProProPheTyr 260
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Qy 261 SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr 280
Db 730 TCCAACACGGGCCAGGCCATCTCCCCGGGATGAAGAGGAGGATTCGCCCTGGGCGCATC 789
Qy 281 GluPheProAsnProGluTrpSerGluValSerGluGluValLysMetLeuIleArgAsn 300
Db 790 GGCTTCCCAATCTGAGTGGTCAGAGTCTCTGAGGATGCCAAGCAGCTGATCCGCTC 849
Qy 301 LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTrp 320
Db 850 CTGTTGAAGACAGACCCCAAGAGGCTGACCATCACTCAGTTCAATGAACCAACCCCTGG 909
Qy 321 IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGlu 340
Db 910 ATCAACCAATCGATGGTAGTGCCACAGACCCCACTCCACACGGCGCCGAGTGCTGAGAG 969
Qy 341 AspLysGluArgTrpGluAspValLysGluGluMetThrSerAlaLeuAlaThrMetArg 360
Db 970 GACAAACACCACTGGGACGAGTCAAGAGGAGATGACCATGCTTGGCCCATATGCGG 1029
Qy 361 ValAspTyrGluGlnIleLysIleLysIleGluAspAlaSerAsnProLeuLeuLeu 380
Db 1030 GTAGACTACCAACAGGTGAAGATCAAGGACCTGAAGACCTCTAACACCGGCTCTCAAC 1089
Qy 381 LysArgArgLysLysAlaAaArgAlaLeuGluAlaAla 393
Db 1090 AAGAGGAGAAAAAGAGCGGCGAGCTCTCTCTGCTCA 1128
RESULT 10
LOCUS CR606251 1799 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CSODI054YL13 of Placenta Cot 25-normalized
of Homo sapiens (human).
ACCESSION CR606251
VERSION CR606251.1 GI:50487058
KEYWORDS HTC; cDNA.
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1 (bases 1 to 1799)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue
REFERENCE 2 (bases 1 to 1799)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES             Location/Qualifiers
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ORIGIN
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Score:              1391.00        Matches:        265
Percent Similarity: 80.2%          Conservative:   50
Best Local Similarity: 67.4%       Mismatches:    56
Query Match:        66.0%          Indels:        22
DB:                  Gaps:         3
US-10-469-221-2 (1-396) x CR606251 (1-1799)
Qy 1 SerGlnGlyGlnSerProValProPheProAlaProAlaProGlnProPro 20
Db 126 GCAGAGAGCAGGGGGGCGCTGTGCCC-----CGCCAGTTGCACCGCGC 170
Qy 21 ThrProAlaLeuProHisProProAlaGlnProProProProGlnGlnPhePro 40
Db 171 GGACCGCGCTGGCGCGTGTCTCGGGGGGGCGCGGAGGCC----- 212
Qy 41 GlnPheHisValLysSerGlyLeuGlnIleLysLysAsnAlaIleLeuAspTyrLys 60
Db 213 -----AAGAGTACGACGATGACCGACGACTACCGAG 242
Qy 61 ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLys 80
Db 243 TTGTCCAGCAGGTGCTGGCGCTGGGTGGAACGCAAGTGTGGAGTCTTCCATCGG 302
Qy 81 ArgThrGlnGlnLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaAaArgGlu 100
Db 303 CGCACTGGACAGAAGTGTGCCCTGAAGTCTCTGTATGACAGGCCCAAGGCCCGCGAGAG 362
Qy 101 ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr 120
Db 363 GTAGACCATCAGTGGCAGGCTCTGCGGCCCCCATATTGTCGATCTGGAGTGTAT 422
Qy 121 GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly 140
Db 423 GAGAACATGCACCATGGAAGCGCTGTCTCTCATCATCATGATGATGGAAGGTGT 482
Qy 141 GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer 160
Db 141
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Db 483 GAGTGTTCAGCAGGATTTCAGGAGCGTGGCGCACCAGCGCTTTCACCTGAGAGAGAGCTGCA 542
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Db 543 GAGATATCGGGATATTGGCACTGCCATCCAGTTCGACAGCCATTAACATTTGCCAC 602
Qy 181 ArgAspValLysProGluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeuLys 200
Db 603 CGAGATGTCAGGCTGAAACCTACTCTACACATCTAAGGAGAAAGACGCGAGTGTCTTAAG 662
Qy 201 LeuThrAspPheGlyPheAlaLysGlnThrThrSerHisAsnSerLeuThrThrProCys 220
Db 663 CTCACCGATTTCGCTTTCGTAAGAGACACCC---CAAAATGCGCTTCAGACACCCCTGC 719
Qy 221 TyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys 240
Db 720 TATACTCCCTATTATGTGGCCCTTGAGTCTGGTCCAGAGAGATGACAAAGTCATGT 779
Qy 241 AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProProPheTyr 260
Db 780 GACATGTGGTCCCTGGGTGCATCATGTACATCCTCTTGTGGCTTCCACCCCTTCTAC 839
Qy 261 SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr 280
Db 840 TCCAACACGGGCCAGGCCATCTCCCGGGGATGAGAGAGAGATTCGCTGGGCCAGTAC 899
Qy 281 GluPheProAsnProGluTrpSerGluValSerGluGluValLysMetLeuIleArgAsn 300
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Qy 301 LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTrp 320
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Qy 381 LysArgLysLysAlaArgAlaLeuGluAlaAla 393
Db 1200 AAGAGGAGAAAAAGCAGGCGAGCTCTCTGCTCA 1238

RESULT 11
LOCUS BC068497 3003 bp mRNA linear HTC 25-JUN-2004
DEFINITION Homo sapiens mitogen-activated protein kinase-activated protein
kinase 3, mRNA (cDNA clone IMAGE:4823572).
ACCESSION BC068497
VERSION BC068497.1 GI:46329920
KEYWORDS HTC
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 3003)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, W.J., Ustin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J.,

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McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Faney, J., Helton, E., Kettman, M., Madan, A., Young, A.C., Shvachenko, Y.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shvachenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalek, U., Smilus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
REFERENCE
2 (bases 1 to 3003)
Strausberg, R.
Direct Submission
Submitted (02-APR-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapb-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAC Plate: 167 Row: f Column: 16
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 14589907
This clone has the following problem: clone inconsistent with known
gene structure.
FEATURES
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Alignment Scores:
Pred. No.: 4.18e-108 Length: 3003
Score: 1384.00 Matches: 261
Percent Similarity: 80.5% Conservative: 49
Best Local Similarity: 67.8% Mismatches: 55
Query Match: 65.7% Indels: 20
DB: 6 Gaps: 2
US-10-469-221-2 (1-396) x BC068497 (1-3003)
Qy 9 ProPheProAlaProAlaProGlnProProThrProAlaLeuProHisProPro 28
Db 630 CCTGTGCCCCCAGCAGTTGCACCGGCGGCGGTTCGGCGGGGGCGG 689
Qy 29 AlaGlnProProProProProGlnGlnPhePheHisValLysSerGlyLeu 48
Db 690 CGGAGAGCCC----- 698
Qy 49 GlnIleLysLysAsnAlaIleIleAspTyrLysValThrSerGlnValLeuGlyLeu 68

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Db 699 -----AAGAAGTACGCAGTGCACGACGACTACAGCTTGCTCCAAAGCAGGTCGTGGGCGTG 752
Qy 69 GlyIleAsnGlyIysValLeuGlnIlePheAsnLysArgThrGlnGluLysPheAlaLeu 88
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Qy 89 LysMetLeuGlnAspCysProLysAlaArgGluValGluLeuHisTrpArgAlaSer 108
Db 813 AAGCTCTCTATGACACGCCCAAGCCGCGGAGGAGGTAGACCATCTACCTGGCAGGCTTCT 872
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Qy 129 CysLeuLeuIleValMetGluCysLeuAspGlyGlyLeuIlePheSerArgIleGlnAsp 148
Db 933 TGTCTCTCATCATCATGGAATGATGCAAGAGTGTGAGTTGTTTCAGCAGGATTCAGGAG 992
Qy 149 ArgGlyAspGlnAlaPheThrGluArgGluAlaSerGluIleMetLysSerIleGlyGlu 168
Db 993 CGTGGCCACGAGGCTTTCTACTGAGAGAGAAGCTGCAGAGATAATGCGGATATTGGCACT 1052
Qy 169 AlaIleGlnTyrLeuHisSerIleAsnIleAlaHisArgAspValLysProGluAsnLeu 188
Db 1053 GCCATCCAGTTCTGCACAGCCATAACATTGCCACCAGAGATGTCGAAGCTGAAACCTA 1112
Qy 189 LeuTyrThrSerLysArgProAsnAlaIleLeuLysLeuThrAspPheGlyPheAlaLys 208
Db 1113 CTCTACACATCTAAGGAGAAAGACGAGTGTAAAGCTCACCGATTTTGGCTTTGCTAAG 1172
Qy 209 GluThrThrSerHisAsnSerLeuThrThrProCysTyrThrProTyrTyrValAlaPro 228
Db 1173 GAGACCAACC---CAAAATGGCCCTGCACACACCTTCTATCTATCTATATATGGCCCCCT 1229
Qy 229 GluValLeuGlyProGluLysTyrAspLysSerCysAspMetTrpSerLeuGlyValIle 248
Db 1230 GAGTCTCTGGTCCAGAGAAGTATGACAAGTCATGTGCATGTGTCCTCGGTGTGTCATC 1289
Qy 249 MetTyrIleLeuLeuCysGlyTyrProProPheTyrSerAsnHisGlyLeuAlaIleSer 268
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Qy 269 ProGlyMetLysThrArgIleAtqMetGlyGlnTyrGluPheProAsnProGluTyrSer 288
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Qy 289 GluValSerGluGluValLysMetLeuIleArgAsnLeuLysThrGluProThrGln 308
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Qy 309 ArgMetThrIleThrGluPheMetAsnHisProTrpIleMetGlnSerThrLysValPro 328
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Qy 329 GlnThrProLeuHisThrSerArgValLeuLysAspLysGluArgTyrGluAspVal 348
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Qy 369 LysLysIleGluAspAlaSerAsnProLeuLeuLysArgArgLysLysAlaArgAla 388
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AY403349
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RESULT 12  
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LOCUS

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DEFINITION Mus musculus MAPKAPK3 gene, VIRTUAL TRANSCRIPT, partial sequence,  
genomic survey sequence.  
ACCESSION AY403349  
VERSION AY403349.1 GI:39759332  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidae; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 1155)  
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferrieri,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering  
them based on alignment.  
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/locus_tag="HCM1527"  
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Alignment Scores:  
Pred. No.: 1.13e-106 Length: 1155  
Score: 1361.00 Matches: 258  
Percent Similarity: 80.7% Conservative: 51  
Best Local Similarity: 67.4% Mismatches: 48  
Query Match: 64.6% Indels: 26  
DB: 14 Gaps: 3  
US-10-469-221-2 (1-396) x AY403349 (1-1155)  
Qy 19 ProProThrProAlaLeu-----ProHisProProAlaGln 30  
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Db 100 CGGGAACCC-----108  
Qy 51 LysGlyAsnAlaIleIleAspTyrLysValThrSerGlnValLeuGlyLeuGlyIle 70  
Db 109 AAGAAGTACCGGTGACTGATGACTACCACTTGTCCAAGCAAGTGTGGGTCTGGGTGTG 169  
Qy 71 AsnGlyLysValLeuGlnIlePheAsnLysArgThrGlnGluLysPheAlaLeuLysMet 90  
Db 169 AACGGCAAGGTACTGGAGTGTCTACCATCGCGCTCTGCCAGCAAGTGTGCTTGAAGCTC 228  
Qy 91 LeuGlnAspCysProLysAlaArgGluValGluLeuHisTrpArgAlaSerGlnCys 110  
Db 229 CTGTATGACAGCCCAAGCCCGCAGGAGGTGACCAACCACTGCGAGGCGTCAGGCGGC 288  
Qy 111 ProHisIleValArgIleValAspValTyrGluAsnLeuTyrAlaGlyArgLysCysLeu 130  
Db 289 CCCCACATCTGTCGATCTCTGGACGTGTATGAGATATGACCAACGCAAGCGCTGTCTC 348
```





Itôh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes  
Genome Res. 10 (10), 1617-1630 (2000)  
11042159

3  
Shibata, K., Itôh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,  
Konno, H., Akiyama, J., Nishi, K., Kitsuunai, T., Tashiro, H., Itoh, M.,  
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,  
Yanamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
Fujiwaka, S., Inoue, K., Todawa, Y., Izawa, M., Ohara, E., Watahiki, M.,  
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,  
Okazaki, Y., Muramatsu, M., Inoue, K., Kira, A. and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multipicapillary sequencer  
Genome Res. 10 (11), 1757-1771 (2000)  
11076861

4  
Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,  
Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,  
Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I.,  
Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,  
Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,  
Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H.,  
Kuehl, P., Lewis, S., Matsuo, Y., Nikaïdo, I., Pesole, G.,  
Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M.,  
Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,  
Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,  
Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C.,  
Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,  
Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P.,  
Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P.,  
Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,  
Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H.,  
Toyo-oka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L.,  
Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S.  
and Hayashizaki, Y.  
RIKEN Genome Exploration Research Group Phase II Team and the  
FANTOM Consortium  
Functional annotation of a full-length mouse cDNA collection  
Nature 409 (6821), 685-690 (2001)  
11217851

5  
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,  
Nikaïdo, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,  
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,  
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,  
Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,  
Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusci, V.,  
Ciochia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,  
Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,  
Gariboldi, M., Glissi, C., Godzik, A., Gough, J., Grimmond, S.,  
Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,  
Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Kongaya, A.,  
Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,  
Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,  
Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,  
Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramchandran, S.,  
Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,  
Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,  
Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,  
Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,  
Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,  
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,  
Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,  
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,  
Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,  
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,  
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,  
Rogers, J., Birney, E. and Hayashizaki, Y.  
FANTOM Consortium  
Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs

CONSTRM  
TITLE  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS

JOURNAL  
PUBMED  
REFERENCE  
AUTHORS

Nature 420 (6915), 563-573 (2002)

12466851

6

Carninci, P., Kasukawa, T., Katayama, S., Gough, J., Frith, M.C.,  
Maeda, N., Oyama, R., Ravasi, T., Lenhard, B., Wells, C., Kodzius, R.,  
Shimokawa, K., Bajic, V.B., Brenner, S.E., Batalov, S., Forrest, A.R.,  
Zavolan, M., Davis, M.J., Wilming, L.G., Aidinis, V., Allen, J.E.,  
Ambesi-Impombato, A., Apweiler, R., Aturaliya, R.N., Bailey, T.L.,  
Bansal, M., Baxter, L., Beisel, K.W., Bersano, T., Bono, H., Chalk, A.M.,  
Chiu, K.P., Choudhary, V., Christoffels, A., Clutierbeck, D.R.,  
Crome, M.L., Dalla, E., Dalrymple, B.P., de Bono, B., Della Gatta, G.,  
di Bernardo, D., Down, T., Engstrom, P., Fagiolini, M., Faulkner, G.,  
Fletcher, C.F., Fukushima, T., Furuno, M., Futaki, S., Gariboldi, M.,  
Georgii-Hemming, P., Gingeras, T.R., Gojobori, T., Green, R.E.,  
Gustincich, S., Harbers, M., Hayashi, Y., Hensch, T.K., Hirokawa, N.,  
Hill, D., Huminecki, L., Iacono, M., Ikeo, K., Iwama, A., Ishikawa, T.,  
Kato, M., Kanapin, A., Katoh, M., Kawasawa, Y., Keiso, J., Kitamura, H.,  
Kitano, H., Kollas, G., Krishnan, S.P., Kruger, A., Kummerfeld, S.K.,  
Kurochkin, I.V., Lareau, L.P., Lazarevic, D., Lipovich, L., Liu, J.,  
Liuni, S., McWilliam, S., Madan Babu, M., Madera, M., Marchionni, L.,  
Matsuda, H., Matsuzawa, S., Miki, H., Mignone, F., Miyake, S.,  
Morris, K., Mottagui-Tabar, S., Mulder, N., Nakano, N., Nakauchi, H.,  
Ng, P., Nilsson, R., Nishiguchi, S., Nishikawa, S., Nori, F., Ohara, O.,  
Okazaki, Y., Orlando, V., Pang, K.C., Pavan, W.J., Pavese, G.,  
Pesole, G., Petrovsky, N., Piazza, S., Reed, J., Reid, J.P., Ring, B.Z.,  
Ringwald, M., Rost, B., Ruan, Y., Salzberg, S.L., Sandelin, A.,  
Schnaider, C., Schonbach, C., Sekiguchi, K., Semple, C.A., Seno, S.,  
Sessa, L., Sheng, Y., Shibata, Y., Shimada, H., Shimada, K., Silva, D.,  
Sincalir, B., Sperling, S., Stupka, E., Sugiyara, K., Sultana, R.,  
Takenaka, Y., Taki, K., Tammoja, K., Tan, S.L., Tang, S., Taylor, M.S.,  
Tegner, J., Teichmann, S.A., Ueda, H.R., van Nimwegen, E., Verardo, R.,  
Wei, C.L., Yagi, K., Yamanishi, H., Zabarovsky, E., Zhu, S., Zimmer, A.,  
Hide, W., Bult, C., Grimmond, S.M., Teasdale, R.D., Liu, E.T.,  
Brusci, V., Quackenbush, J., Wahlestedt, C., Mattick, J.S., Hume, D.A.,  
Kai, C., Sasaki, D., Tomaru, Y., Fukuda, S., Kanamori-Katayama, M.,  
Suzuki, M., Aoki, J., Arakawa, T., Iida, J., Imamura, K., Itoh, M.,  
Kato, T., Kawaji, H., Kawagashira, N., Kawashima, T., Kojima, M.,  
Kondo, S., Konno, H., Nakano, K., Ninomiya, N., Nishio, T., Okada, M.,  
Plessey, C., Shibata, K., Shiraki, T., Suzuki, S., Tagami, M., Waki, K.,  
Watahiki, A., Okamura-Ohno, Y., Suzuki, H., Kawai, J. and Hayashizaki, Y.  
FANTOM Consortium  
The transcriptional landscape of the mammalian genome  
Science 309 (5740), 1559-1563 (2005)  
16141072

7  
Katayama, S., Tomaru, Y., Kasukawa, T., Waki, K., Nakanishi, M.,  
Nakamura, M., Nishida, H., Yap, C.C., Suzuki, M., Kawai, J., Suzuki, H.,  
Carninci, P., Hayashizaki, Y., Wells, C., Frith, M., Ravasi, T.,  
Pang, K.C., Hallinan, J., Mattick, J., Hume, D.A., Lipovich, L.,  
Batalov, S., Engstrom, P.G., Mizuno, Y., Faghihi, M.A., Sandelin, A.,  
Chalk, A.M., Mottagui-Tabar, S., Liang, Z., Lenhard, B. and  
Wahlestedt, C.  
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Antisense transcription in the mammalian transcriptome  
Science 309 (5740), 1564-1566 (2005)  
16141073

8 (bases 1 to 2724)  
Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K.,  
Hori, F., Iida, J., Imamura, K., Imotani, K., Itoh, M., Kanegawa, S.,  
Kawai, J., Kojima, M., Konno, H., Murata, M., Nakamura, M., Ninomiya, N.,  
Nishiyori, H., Nomura, K., Ohno, M., Sakazume, N., Sano, H., Sasaki, D.,  
Shibata, K., Shiraki, T., Tagami, M., Tagami, Y., Waki, K., Watahiki, A.,  
Muramatsu, M. and Hayashizaki, Y.  
Direct Submission

TITLE

JOURNAL

Submitted (14-APR-2004) Yoshihide Hayashizaki, The Institute of  
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COMMENT

Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.  
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics  
Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome  
Trust/MRC building Addenbrookes Hospital Cambridge) whose  
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Please visit our web site for further details.  
URL: <http://genome-gsc.riken.jp/>  
URL: <http://fantom.gsc.riken.jp/>.

## FEATURES

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Query Match: 64.6% Indels: 26  
DB: 6 Gaps: 3

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ACCESSION AK151881  
VERSION AK151881.1 GI:74207146  
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Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
REFERENCE 1  
AUTHORS Carninci, P. and Havaehizaki, Y.  
TITLE High-efficiency full-length cDNA cloning  
JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
PUBMED 10349636

- 2  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS
- Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000) 11042159
- 3  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS
- Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, K., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, K., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, K., Oneda, Y., Muramatsu, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Yoneda, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000) 11076861
- 4  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS
- Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesole, G., Quackenbush, J., Schriml, L.M., Stauber, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyooka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y.
- 5  
CONSRMT  
TITLE  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS
- RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium  
Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001) 11217851
- 6  
CONSRMT  
TITLE  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS
- Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaide, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I., Jarvis, E.D., Kanai, A., Kawai, J., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Ravan, W.J., Perte, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Sempke, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Varado, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yangisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kaga, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.
- 7  
CONSRMT  
TITLE  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS
- Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420 (6915), 563-573 (2002) 12466951
- 8  
CONSRMT  
TITLE  
JOURNAL  
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- 9  
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- RIKEN Genome Exploration Research Group  
Antisense transcription in the mammalian transcriptome Science 309 (5740), 1559-1563 (2005) 16141072
- 10  
CONSRMT  
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JOURNAL  
PUBMED  
REFERENCE  
AUTHORS
- Katayama, S., Tomaru, Y., Kasukawa, T., Waki, K., Nakanishi, M., Nakamura, M., Nishida, H., Yap, C.C., Suzuki, M., Kawai, J., Suzuki, H., Carninci, P., Hayashizaki, Y., Wells, C., Frith, M., Ravasi, T., Pang, K.C., Hallinan, J., Mattick, J., Hume, D.A., Lipovich, L., Batalov, S., Engstrom, P.G., Mizuno, Y., Faghihi, M.A., Sandelin, A., Chalk, A.M., Mottagui-Fabriz, S., Liang, Z., Lenhard, B. and Wahlestedt, C.
- 11  
CONSRMT  
TITLE  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS
- RIKEN Genome Exploration Research Group  
Antisense transcription in the mammalian transcriptome Science 309 (5740), 1564-1566 (2005) 16141073
- 12  
CONSRMT  
TITLE  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS
- Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hori, F., Iida, J., Imamura, K., Imotani, K., Itoh, M., Kanagawa, S., Kawai, J., Kojima, M., Konno, H., Murata, M., Nakamura, M., Ninomiya, N., Nishiyori, H., Nomura, K., Ohno, M., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shiraki, T., Tagami, M., Tagami, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y.
- 13  
CONSRMT  
TITLE  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS
- Direct Submission  
Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)







GenCore version 5.1.9  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 19, 2006, 14:41:57 ; Search time 815 Seconds  
(without alignments)  
5081.614 Million cell updates/sec

Title: US-10-469-221-2

Perfect score: 2106

Sequence: 1 SQGSPVPFPAPAPPPQPP.....PLLKRRKKARALEAAALAH 396

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N Geneseq 8.\*

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2: Geneseqn1990s.\*  
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4: Geneseqn2001as.\*  
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7: Geneseqn2002bs.\*  
8: Geneseqn2003as.\*  
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12: Geneseqn2004as.\*  
13: Geneseqn2004bs.\*  
14: Geneseqn2005s.\*  
15: Geneseqn2006s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2106	100.0	1191	8 AAD50036	Human trn
2	2106	100.0	1203	8 AAD50037	Human ful
3	2097	99.6	1203	14 ADV43403	Human psy

4	2097	99.6	1726	12 ADM36339	Adm36339 Human MK2
5	2097	99.6	1726	14 ADX06659	Adx06659 Cyclin-de
6	2078	98.7	1336	6 ABK84657	Abk84657 Human cDN
7	2078	98.7	1336	11 ADI32071	Adi32071 Human cDN
8	2078	98.7	1336	13 ADS84138	Ads84138 Human lym
9	2006.5	95.3	2263	6 ABV73995	Abv73995 Human MAP
10	2006.5	95.3	2263	9 ACA62272	Ac62272 Human DNA
11	2006.5	95.3	2263	12 ADM36337	Adm36337 Human MK2
12	2006.5	95.3	2263	14 ADX06657	Adx06657 Cyclin-de
13	2006.5	95.3	2263	14 ADY86797	Ady86797 Human MAP
14	2006.5	95.3	2263	14 AEA89439	Aea89439 Human MAP
15	2006.5	95.3	3608	14 ADZ49304	Adz49304 Insulin s
16	1991.5	94.6	2258	6 ABL67227	Ab167227 Thyroid c
17	1991.5	94.6	2258	10 ACA56817	Ac56817 Human sig
18	1991.5	94.6	2258	12 ADI56613	Adi56613 Human pol
19	1991.5	94.6	2258	12 ADP87578	Adp87578 Human NOV
20	1991.5	94.6	2258	14 AED17914	Aed17914 Fibrotic
21	1925.5	91.4	2802	3 AAF15803	Aaf15803 Human pro
22	1886	89.6	2592	13 ACN41322	Acn41322 Human dia
23	1882	89.4	1113	14 ADV43402	Adv43402 Human psy
24	1882	89.4	1128	12 ADP87584	Adp87584 Human NOV
25	1870	88.8	1130	12 ADP87582	Adp87582 Human NOV
26	1870	88.8	1133	12 ADP87586	Adp87586 Human NOV
27	1803	85.6	1026	12 ADP87588	Adp87588 Human NOV
28	1729	82.1	1305	9 ACF57389	Acf57389 SUMO-MPAK
29	1720.5	81.7	3186	8 ACC46238	Acc46238 Human dit
30	1716	81.5	981	12 ADN61587	Adn61587 DNA encod
31	1709	81.1	1168	14 AEE13869	Aee13869 Hamster c
32	1552	73.7	885	12 ADP87580	Adp87580 Human NOV
33	1552	73.7	885	12 ADP87590	Adp87590 Human NOV
34	1391	66.0	1149	14 AEE19658	Aee19658 Human MAP
35	1391	66.0	1298	6 ABK84332	Abk84332 Human cDN
36	1391	66.0	2481	6 ABK84214	Abk84214 Human cDN
37	1391	66.0	2481	6 ABK13301	Abk13301 DNA encod
38	1391	66.0	2481	10 ADD14766	Add14766 Human src
39	1391	66.0	2481	10 ACA56490	Ac56490 Human sig
40	1391	66.0	2481	12 ADI56286	Adi56286 Human pol
41	1391	66.0	2481	12 ADO52389	Ado52389 Human BRC
42	1391	66.0	2500	12 ADP21372	Adp21372 Gene MAPK
43	1391	66.0	2500	12 ADQ87216	Adq87216 Human tum
44	1391	66.0	2500	15 AEF92766	Aef92766 Human mit
45	1391	66.0	2509	11 ADN95702	Adn95702 Human BEC

#### ALIGNMENTS

RESULT 1

AAD50036  
ID AAD50036 standard; cDNA; 1191 BP.

XX AC AAD50036;

XX DT 24-MAR-2003 (first entry)

XX DE Human truncated MAPKAP-2 kinase, tdnMAPKAP-2 cDNA.

XX KW Human; mitogen-activated protein kinase activating protein kinase-2;  
XX KW MAPKAP-2 kinase; signal transduction; cell proliferative disorder;  
XX KW immune system disorder; inflammation; arthritis; immunomodulator;  
XX KW cytoskeletal; gene therapy; enzyme; gene; ss.

XX OS Homo sapiens.

XX PH Key Location/Qualifiers

XX FT CDS 1..1191

XX FT /tag= a

XX FT /product= "Human tdnMAPKAP-2"

XX FT /note= "No start codon"

XX FT /partial

XX PN WO200290524-A2.

XX PD 14-NOV-2002.

```

XX 25-FEB-2002; 2002WO-US005670.
PF
XX
XX 28-FEB-2001; 2001US-0272260P.
PR
XX
XX (MERI ) MERCK & CO INC.
PA
XX
XX Lograsso P, Hawkins J, Linscock JM;
PI
XX WPI; 2003-111970/10.
DR
XX P-PSDB; AAE29898.
DR
XX
XX New isolated nucleic acid molecule encoding a human mitogen-activated
PT protein kinase activating protein kinase-2 (MAPKAP-2), useful for
PT treating immune-system related disorders, inflammation and arthritis.
XX
XX Claim 1; Fig 1; 150pp; English.
PS
XX
XX The invention relates to an isolated nucleic acid molecule comprising a
CC sequence of nucleotides that encode a human mitogen-activated protein
CC kinase activating protein kinase-2 (MAPKAP-2 kinase) and a coding region
CC that encodes a splice variant of a MAPKAP-2 kinase. The invention is
CC especially useful in regulating signal transduction in a cell and in
CC diagnosing or treating MAPKAP-2-mediated disorders eg. cell proliferative
CC disorders, immune system disorders, inflammation, arthritis. The nucleic
CC acid and the polypeptide may also be used in screening assays, predictive
CC medicine, diagnostic or prognostic assays, chromosome mapping, tissue
CC typing, pharmacogenomics and in monitoring clinical trials. The invention
CC is useful in gene therapy. The present sequence is human truncated MAPKAP
CC -2 kinase, tónaMAPKAP-2 cDNA
XX
XX Sequence 1191 BP; 300 A; 362 C; 311 G; 218 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 1.53e-141 Length: 1191
Score: 2106.00 Matches: 396
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 8 Gaps: 0
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QY 1 SerGlnGlyGlnSerProValProPheProAlaProAlaProProGlnProPro 20
DB 1 TCCAGGGCCAGAGCCCGCGGGTCCGTTCCTCCGCGCCCGCGCGCGCGCGCGCGCC 60
QY 21 ThrProAlaLeuProHisProAlaGlnProProProProProProGlnGlnPhePro 40
DB 61 ACCCTGCTCCGCGACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
QY 41 GlnPheHisVallySerGlyLeuGlnIleLysLysAsnAlaIleLeleAspTyrLys 60
DB 121 CAGTTCACGTCAAGTCCGCGCTGCAGATCAAGAAGAACGCCATCATCGATGACTACAAG 180
QY 61 ValThrSerGlnValLeuGlyLeuGlyLysAsnGlyLysValLeuGlnIlePheAsnLys 80
DB 181 GTCACAGCAGGAGGCTCGGGGCTGGGCATCAACGGCAAGATTTGCGAGATCTTCAACAAG 240
QY 81 ArgThrGlnGlyLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaArgArgGlu 100
DB 241 AGNACCCAGAGAAATTCGGCTCAAAATGCTTCAGGACTGCCCCAAGGCCCGCAGGGAG 300
QY 101 ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr 120
DB 301 GTGGAGCTGCACTGGCGGGGCTCCAGTGGCCGACATCGTACGGATCGTGGATGTGTAC 360
QY 121 GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly 140
DB 361 GAGNATCTGTACCGAGGAGAGTGCCTGCTGATGCTCATGGNATGTTTGGACGGTGA 420
QY 141 GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer 160

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DB 421 GAACTCTTTAGCCGAATCCAGGATCCAGGAGACCAGGCATTCACAGAAAGAGAGCATCC 480
QY 161 GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis 180
DB 481 GAAATCATGAAGAGCATCGGTGAGGCATCCAGTATCTGCATTCAATCAATTCGCCCAT 540
QY 181 ArgAspVallyProGluAsnLeuTyrThrSerLysArgProAsnAlaIleLeuLys 200
DB 541 CGGGATGTCAAGCCTGAGAAATCTTTATACACCTCCAAAAGGCCCAACGCCATCTGAAA 600
QY 201 LeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCys 220
DB 601 CTCACGTGACTTTGGCTTTGCCAAGGAAACACCAGGCACAACTCTTTGACCACTCTTGT 660
QY 221 TyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys 240
DB 661 TATACACCGTACTATCTGCTCCAGAAAGTCTGGTCCAGAGAAGTATGACAAGTCTCTGT 720
QY 241 AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProProPheTyr 260
DB 721 GACATGTGGTCCCTGGGTGTATCATGTATCATCTCTGTGTGGGTATCCCCCTTCTAC 780
QY 261 SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr 280
DB 781 TCCAAACCCGGCTTCCCATCTCTCCGGGCATGAGACTCGCATCCGAATGGGCCAGTAT 840
QY 281 GluPheProAsnProGluTrpSerGluValSerGluValLysMetLeuIleArgAsn 300
DB 841 GAATTTTCCCAACCCAGAAATGCTCAGAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT 900
QY 301 LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTyr 320
DB 901 CTGCTGAAACAGAGCCCGCCAGAGAAATGACCATCAGGAGTTTATGAACACCCCTTGG 960
QY 321 IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGlu 340
DB 961 ATCATGCAATCAACAAAGGTCCCTCAACCCCACTCACACACGCGGTCTCTGAAGGAG 1020
QY 341 AspLysGluArgTrpGluAspVallyLysGluLysMetThrSerAlaLeuAlaThrMetArg 360
DB 1021 GACAAGGCGGTGGGAGGATGTCGAAGGAGGAGATCACCAGTGCCTTGGCCACAATGCGC 1080
QY 361 ValAspTyrGluGlnIleLysLysIleGluAspAlaSerAsnProLeuLeuLeu 380
DB 1081 GTTGACTACGAGCAGATCAAGATAAAAAGATTGAAGTGCATCCAAACCTCTGCTGCTG 1140
QY 381 LysArgArgLysLysAlaArgAlaLeuGluAlaAlaLeuAlaHis 396
DB 1141 AAGAGGCGGAAGAAAGCTCGGGCCCTGGAGGCTCGGGCTCTGGCCAC 1188
RESULT 2
AAD50037
ID AAD50037 standard; cDNA; 1203 BP.
XX
XX AAD50037;
XX
XX 24-MAR-2003 (first entry)
DT
DE Human full length MAPKAP-2 kinase, fldnaMAPKAP-2 cDNA.
XX
XX Human; mitogen-activated protein kinase activating protein kinase-2;
KW MAPKAP-2 kinase; signal transduction; cell proliferative disorder;
KW immune system disorder; inflammation; arthritis; immunomodulator;
KW cytoskeletal; gene therapy; enzyme; gene; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..1203
XX FT /tag= a
XX FT /product= "Human fldnaMAPKAP-2"
XX
XX WO200290524-A2.

```

XX 14-NOV-2002.  
 PD 25-FEB-2002; 2002WO-US005670.  
 XX 28-FEB-2001; 2001US-0272260P.  
 PR (MERI ) MERCK & CO INC.  
 XX Lograsso P, Hawkins J, Lisnock JM;  
 PI WPI; 2003-111970/10.  
 XX P-PSDB; AAE29899.  
 DR New isolated nucleic acid molecule encoding a human mitogen-activated  
 PT protein kinase activating protein kinase-2 (MAPKAP-2), useful for  
 PT treating immune-system related disorders, inflammation and arthritis.  
 XX Claim 63; Fig 3; 150pp; English.  
 CC The invention relates to an isolated nucleic acid molecule comprising a  
 CC sequence of nucleotides that encode a human mitogen-activated protein  
 CC kinase activating protein kinase-2 (MAPKAP-2 kinase) and a coding region  
 CC that encodes a splice variant of a MAPKAP-2 kinase. The invention is  
 CC especially useful in regulating signal transduction in a cell and in  
 CC diagnosing or treating MAPKAP-2-mediated disorders eg. cell proliferative  
 CC disorders, immune system disorders, inflammation, arthritis. The nucleic  
 CC acid and the polypeptide may also be used in screening assays, predictive  
 CC medicine, diagnostic or prognostic assays, chromosome mapping, tissue  
 CC typing, pharmacogenomics and in monitoring clinical trials. The invention  
 CC is useful in gene therapy. The present sequence is human full length  
 CC MAPKAP-2 kinase, fldnaMAPKAP-2 CDNA  
 XX SQ Sequence 1203 BP; 303 A; 366 C; 313 G; 221 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 1.55e-141 Length: 1203  
 Score: 2106.00 Matches: 396  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: 8 Gaps: 0

US-10-469-221-2 (1-396) x AAD50037 (1-1203)

QY 1 SerGlnGlyGlnSerProProValProPheProAlaProAlaProProGlnProPro 20  
 DB 13 TCCACAGGCGCAGAGCCCGCGGTGCGTTCCTCCCGCCCGCGCCCGCGAGCCCCC 72

QY 21 ThrProAlaLeuProHisProProAlaGlnProProProProProProGlnGlnPhePro 40  
 DB 73 ACCCTGCGCTGCGCGACCCCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 132

QY 41 GlnPheHisValLysSerGlyLeuGlnGlnLysLysAsnAlaAlaAlaAlaAlaAla 60  
 DB 133 CAGTTCACGTCAGTCCGGCTGCGATCAAGAGAGAGCGCCATCATCGATGACTACAG 192

QY 61 ValThrSerGlnValLeuGlyLeuGlyLeuGlyLeuGlyLeuGlyLeuGlyLeuGlyLeu 80  
 DB 193 GTCACAGCCAGGTCCTGGGGTGGGCATCAACGGCAAAAGTTTTCAGATCTTCAACAAG 252

QY 81 ArgThrGlnGluLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaArgGlu 100  
 DB 253 AGGACCCAGAGAGAAATTCGCTCAAAATGCTTCAGGACTCGCCCAAGGCCCGCAGGGAG 312

QY 101 ValGluLeuHisTrpArgAlaSerGlnCysProHisLysLysLysLysLysLysLysLys 120  
 DB 313 GTGGAGCTGCACTGGCGGGCTCCCGATGCGCGCACATCGTAGCGATCGTAGTGTGATC 372

QY 121 GluAsnLeuTyrAlaGlyArgLysCysLeuLeuLysLysLysLysLysLysLysLysLys 140  
 DB 373 GAGAATCTGTATCGCAGGAGGAGAGTGCCTGCTGTGATGTGTGATGTGTGATGTGTGATG 432

QY 141 GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer 160  
 DB 433 GAACCTCTTTAGCCGAATCCAGGATCGAGGAGACAGGCAATTCACAGAAAGAGAGCATCC 492

QY 161 GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis 180  
 DB 493 GAAATCATGAAGAGCATCGGTGAGCCATCTGCATTCATCAATCAATCAATCAATCAATCAAT 552

QY 181 ArgAspValLysProGluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeuLys 200  
 DB 553 CGGGATGTCAAGCCTGAGAATCTTTATACACCTCCAAAGGCCCAACGCCATCTCTGAAA 612

QY 201 LeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCys 220  
 DB 613 CTCACTGACCTTGGCTTGGCCAGAGAAACACACGACCAACTCTTTGACCACTCTTGT 672

QY 221 TyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys 240  
 DB 673 TATACACCGTACTATGTGGCTCCAGAAAGTGTGGGTCCAGAGAAAGTATGACAAAGTCCTGT 732

QY 241 AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProPheTyr 260  
 DB 733 GACATGTGGTCCCTGGGTGTTCATCATGTACATCTCTGTGTGGGTATCCCCCTTCTAC 792

QY 261 SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr 280  
 DB 793 TCCAACCAAGCCCTTGCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 852

QY 281 GluPheProAsnProGluTrpSerGluValSerGluGluValLysMetLeuIleArgAsn 300  
 DB 853 GAATTTCCCAACCCAGAAATGTGTCAAGAGTATCAAGAGAAAGTGAAGATGCTCATTCGGGAAT 912

QY 301 LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTrp 320  
 DB 913 CTGCTGAAACAGAGAGCCACCCAGAGAAATGACCATCACCGAGTTTATGAACACCCCTGG 972

QY 321 IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGlu 340  
 DB 973 ATCATGCAATCAACAAAGGTCCCTCAAAACCCCACTGTCACACACCCAGCCGGTCTGAAGAG 1032

QY 341 AspLysGluArgTrpGluAspValLysGluGluMetThrSerAlaLeuAlaThrMetArg 360  
 DB 1033 GACAAGAGCGGTGGGAGGATGTCAAGAGAGAGATGACCATGCTGCTTGGCCCAATGCGC 1092

QY 361 ValAspTyrGluGlnIleLysLysLysLysLysLysLysLysLysLysLysLysLysLys 380  
 DB 1093 GTTCACTACGAGCAGATCAAGATAAAAAGATTGAAGATGATCCAAACCCCTCTGCTGCTG 1152

QY 381 LysArgArgLysLysAlaArgAlaLeuGluAlaAlaAlaAlaAlaHis 396  
 DB 1153 AAGAGCGGAAGAAAGCTCGGGCCCTGGAGGCTCGGCTCTGGGCCAC 1200

RESULT 3  
 ADV43403  
 ID ADV43403 standard; cDNA; 1203 BP.  
 XX  
 AC ADV43403;  
 XX  
 DT 10-MAR-2005 (first entry)  
 XX  
 DE Human psychoneuroendocrinimmune expressed sequence tag SEQ ID NO 1031.  
 XX  
 KW microarray; psychoneuroendocrinimmune; chronic fatigue;  
 KW non-insulin dependent diabetes; allergy; immune disorder; inflammation;  
 KW cancer; neoplasm; infection; expressed sequence tag; ss.  
 OS Homo sapiens.  
 XX  
 PN WO2004108899-A2.  
 XX  
 PD 16-DEC-2004.  
 XX  
 PF 04-JUN-2004; 2004WO-US017686.

```
XX 04-JUN-2003; 2003US-0475915P.
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX Nicholson A, Vernon SD;
XX WPT; 2005-031682/03.
XX
XX New microarray comprising probes for genes involved in
XX psychoneuroendocrine (PNI) activity, useful in diagnosing a
XX condition associated with PNI activity, e.g., inflammatory or infectious
XX diseases.
XX
XX Claim 1; SEQ ID NO 1031; 254pp; English.
XX
XX The invention relates to a new microarray which comprises probes for
XX genes involved in psychoneuroendocrine (PNI) activity. The
XX microarray is useful in diagnosing a condition associated with PNI
XX activity, such as CFS, type-2 diabetes, allergic condition, inflammation,
XX cancer and infection. The present sequence represents a
XX psychoneuroendocrine gene expressed sequence tag. Note the
XX specification mentions SEQ ID NO of up to 3314 but only sequences up to
XX SEQ ID NO 1829 are provided.
XX
XX Sequence 1203 BP; 303 A; 365 C; 313 G; 222 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 6.83e-141 Length: 1203
XX Score: 2097.00 Matches: 395
XX Percent Similarity: 99.7% Conservative: 0
XX Best Local Similarity: 99.7% Mismatches: 1
XX Query Match: 99.6% Indels: 0
XX DB: 14 Gaps: 0
XX
XX US-10-469-221-2 (1-396) x ADV43403 (1-1203)
XX
XX QY 1 SerGlnGlyGlnSerProValProPheProAlaProAlaProProGlnProPro 20
XX DB 13 TCCAGGGCCAGAGCCCGCGGTGCTTCCCGCCCGCGCGCGCGCGCGCGCGCGCG 72
XX
XX QY 21 ThrProAlaLeuProHisProProAlaGlnProProProProGlnGlnPhePro 40
XX DB 73 ACCCTGCTGCGCACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 132
XX
XX QY 41 GlnPheHisValLysSerGlyLeuGlnIleLysLysAsnAlaIleLeuAspTyrLys 60
XX DB 133 CAGTTCCACGTCAAGTCCGCGCTGCAGATCAAGAAGAACGCCATCATCGATGACTACAAG 192
XX
XX QY 61 ValThrSerGlnValLeuGlyLeuGlyLeuGlyLeuGlyValLeuGlnIlePheAsnLys 80
XX DB 193 GTCACAGCAGGTCCTGGGGCTGGGGCATCAACGGCAAGTTTTCAGATCTTCAACAG 252
XX
XX QY 81 ArgThrGlnGluLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaAraArgGlu 100
XX DB 253 AGGACCCAGAGAAATTCGCCCTCAAAATGCTTCAGGACTGCCCAAGGCCCGCAGGGAG 312
XX
XX QY 101 ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr 120
XX DB 313 GTGGAGTGCACGTGGCGGGCTCCACGTGCCCGCACATCGTACGGATCGTGGATGTGTAC 372
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XX QY 121 GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly 140
XX DB 373 GAGNATCTGTACCGAGGAGGAGAGTGTCTGCTGATGTCATGATGTTGGACGCTGGA 432
XX
XX QY 141 GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer 160
XX DB 433 GAACCTTTAGCCGAATCCAGGATCCGAGGACCGAGCAATTCACAGAAAGAGAGCATCC 492
XX
XX QY 161 GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis 180
XX DB 493 GAAATCATGAAGAGCATCGGTGGGGCCATCCAGTATCTGCATTCATCAATCAACATGGCCAT 552
XX
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QY 181 ArgAspValLysProGluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeuLys 200
DB 553 CGGGATGTCAAGCCTCAGAAATCTTATACACCTCCAAAAGGCCCAACGCCATCCTGAAA 612
QY 201 LeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCys 220
DB 613 CTCACCTGACTTTGGCTTTGCCAAGGAAACCAACAGCCACCAACTCTTTGACCACTCTTGT 672
QY 221 TyrThrProTyrTrpValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys 240
DB 673 TATACACCGTACTATCTGGCTCCAGAAAGTCTGGTCCAGAGAGTATGACAAAGTCTCTGT 732
QY 241 AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProProPheTyr 260
DB 733 GACATGTGGTCCCTGGGTGTATCATGTATCTCTGTGTGGGTATCCCCCTTCTCTAC 792
QY 261 SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr 280
DB 793 TCCAACACCGCCTTGCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 852
QY 281 GluPheProAsnProGluTrpSerGluValSerGluValLysMetLeuIleArgAsn 300
DB 853 GAATTTCCCAACCCAGAAATGGTCAGAAATATCAGAGGAAAGTGAAGATGCTCATTCGGAAT 912
QY 301 LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTyr 320
DB 913 CTGCTGAAAACAGAGGCCACCCAGAGAAATGACCATCACCAGTTTATGAACCAACCTTGG 972
QY 321 IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGlu 340
DB 973 ATCATGCAATCAACAAAGGTCCCTCAACCCCACTGCACACAGCGGGTCTTGAAGGAG 1032
QY 341 AspLysGluArgTrpGluAspValLysGluGluMetThrSerAlaLeuAlaThrMetArg 360
DB 1033 GACAAGGAGCGGTGGAGGATGTGCAAGGAGGAGATGACCATGCTGCTGGCCACAAATGCCG 1092
QY 361 ValAspTyrGluGlnIleLysLysIleGluAspAlaSerAsnProLeuLeuLeu 380
DB 1093 GTTGACTACGACGAGATCAAGATATAAAGATTGAAGATGATCCAAACCTCTGCTGCTG 1152
QY 381 LysArgArgLysLysAlaArgAlaLeuGluAlaAlaAlaAlaHis 396
DB 1153 AAGAGCGGAAAGAAAGCTCGGGCCCTGGAGGCTCGGGCTCTGGCCAC 1200
XX
XX RESULT 4
XX ADM36339
XX ID ADM36339 standard; cDNA; 1726 BP.
XX AC ADM36339;
XX XX
XX DT 03-JUN-2004 (first entry)
XX XX
XX DE Human MK2 variant 2 encoding cDNA SEQ ID NO:3.
XX
XX KW ischaemic injury;
XX KW mitogen-activated protein kinase-activated protein kinase 2; MK2;
XX KW vasotropic; cerebroprotective; cardiac; hypotensive;
XX KW antiatherosclerotic; thrombolytic; neuroprotective; cardiovascular;
XX KW antianimal; antiarrhythmic; MK2 antagonist; cerebral ischaemia;
XX KW ischaemia; vascular occlusion; cerebral infarction; stroke;
XX KW cerebral vascular disease; myocardial infarction;
XX KW coronary artery disease; congestive heart failure; cardiac arrhythmia;
XX KW unstable angina; high blood pressure; claudication;
XX KW peripheral occlusive arterial disease; atherosclerosis;
XX KW thrombotic condition; thromboembolic condition; CNS disorder; human;
XX KW MK2 variant 2; chromosome 1q32; gene; ss.
XX OS Homo sapiens.
XX
XX PH Key Location/Qualifiers
XX FT CDS 379..1581
XX FT /*tag= a
XX FT /product= "MK2 variant 2"
```

XX WO2004017909-A2.  
 XX 04-MAR-2004.  
 XX 21-AUG-2003; 2003WO-US026337.  
 XX 23-AUG-2002; 2002US-0405586P.  
 XX (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 XX  
 XX Wang X, Schieven G, Feuerstein GZ;  
 XX WPI; 2004-226726/21.  
 XX P-PSDB; ADM36340.  
 XX  
 XX Reducing or treating ischemic injury, comprises administering an  
 XX inhibitor of mitogen-activated protein kinase-activated protein kinase 2  
 XX (MK2) activity or expression.  
 XX  
 XX Disclosure; SEQ ID NO 3; 39pp; English.  
 XX  
 XX The present invention describes a method for reducing ischaemic injury in  
 XX a mammal, which comprises administering a compound that reduces the  
 XX activity of mitogen-activated protein kinase-activated protein kinase 2  
 XX (MK2) or that inhibits MK2 expression. Also described: (1) identifying a  
 XX compound which inhibits MK2 expression in a cell, or which modulates MK2  
 XX activity; (2) compounds identified by the method above; and (3) treating  
 XX ischaemic injury by administering to a patient a compound above, or an  
 XX MK2 modulator. The compound has vasotropic, cerebroprotective, cardiac,  
 XX hypotensive, antiarteriosclerotic, thrombolytic, neuroprotective,  
 XX cardiovascular, antianginal and antiarrhythmic activities, and can be  
 XX used as an MK2 antagonist. The method is useful reducing or treating  
 XX ischaemic injury, particularly cerebral ischaemia. Compounds identified  
 XX by the method are useful for treating ischaemia, (e.g. ischaemia  
 XX resulting from vascular occlusion, cerebral infarction, stroke, and  
 XX related cerebral vascular diseases), myocardial infarction, coronary  
 XX artery disease, congestive heart failure, cardiac arrhythmias, unstable  
 XX angina, high blood pressure, claudication, peripheral occlusive arterial  
 XX disease, atherosclerosis, thrombotic or thromboembolic conditions, or CNS  
 XX disorders associated with cerebral ischaemia. The present sequence  
 XX encodes the human MK2 variant 2, which is located on chromosome 1q32.  
 XX  
 XX SQ Sequence 1726 BP; 411 A; 543 C; 481 G; 291 T; 0 U; 0 Other;  
 XX

Alignment Scores:  
 Pred. No.: 1.02e-140 Length: 1726  
 Score: 2097.00 Matches: 395  
 Percent Similarity: 99.7% Conservative: 0  
 Best Local Similarity: 99.7% Mismatches: 1  
 Query Match: 99.6% Indels: 0  
 DB: 12 Gaps: 0

US-10-469-221-2 (1-396) x ADM36339 (1-1726)

Db 631 AGGACCAGGAGAAATTCGCCCTCAAAATGCTTCAGGACTGCCCAAGGCCGAGGAG 690  
 Qy 101 ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr 120  
 Db 691 GTGGAGCTGCACCTGGCGGGCTCCAGTGGCCCGACATCGTACGATCGTGATGTGTAC 750  
 Qy 121 GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly 140  
 Db 751 GAGAATCTGTACGAGGAGGAGAGTGCCTGCTGATTGTCATGGAATGTTTGGACGGTGA 810  
 Qy 141 GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer 160  
 Db 811 GAACTCTTTAGCCGAATCCAGGATCGAGGAGACAGGCATTCACAGAAAGAGAGCATCC 870  
 Qy 161 GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis 180  
 Db 871 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCATCAACATTTGCCCAT 930  
 Qy 181 ArgAspValLysProGluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeuLys 200  
 Db 931 CGGGATGTCAGGCTGAGAATCTCTTATACACCTCCAAAGGCCCAACGCCATCTCTGAAA 990  
 Qy 201 LeuThrAspPheGlyPheAlaLysGluThrThrSerHisSerLeuThrThrProCys 220  
 Db 991 CTCACCTGACTTTGGCTTTGGCAAGAAACACCCAGCCACCAACTCTTTGACCACTCTTGT 1050  
 Qy 221 TyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys 240  
 Db 1051 TATACACCGTACTATGTGGCTCCAGAAAGTGTGGTCCAGAGAGTATGACAACTCTTGT 1110  
 Qy 241 AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProProPheTyr 260  
 Db 1111 GACATGTGGTCCCTGGGTGTCAATCATGTACATCTGCTGTGGTATCCCCCTTCTAC 1170  
 Qy 261 SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr 280  
 Db 1171 TCCAAACACGCGCTTGCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCGCAT 1230  
 Qy 281 GluPheProAsnProGluTyrSerGluValSerGluGluValLysMetLeuIleArgAsn 300  
 Db 1231 GAATTTCCCAACCCAGAAATGCTCAGAAAGTATCAGAGGAGTGAAGATGCTCATTTCCGA 1290  
 Qy 301 LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTrp 320  
 Db 1291 CTGCTGAAAACAGAGCCCAACCCAGAGAATGACCATCACCCAGTTTATGAACCACTTGG 1350  
 Qy 321 IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGlu 340  
 Db 1351 ATCATGCAATCAACAAAGGTCCCTCAAAACCCACTGCACACCCAGCGGGTCTCTGAAGG 1410  
 Qy 341 AspLysGluArgTrpGluAspValLysGluGluMetThrSerAlaLeuAlaThrMetArg 360  
 Db 1411 GACAAGGCGGTGGGAGGATGTCAGGAGAGATGACCATGCTTGGCCACATATCGC 1470  
 Qy 361 ValAspTyrGluGlnIleLysIleLysLysIleGluAspAlaSerAsnProLeuLeuLeu 380  
 Db 1471 GTTGACTACGAGCAGATCAAGATAAAGATTGAAGATGCATCCCAACCTCTGCTCTG 1530  
 Qy 381 LysArgArgLysLysAlaArgAlaLeuGluAlaAlaLeuAlaHis 396  
 Db 1531 AAGAGCGGAAGAAAGCTCGGGCCCTGGAGGCTCGCGCTCTGGCCAC 1578  
 XX  
 XX RESULT 5  
 XX ADX06659  
 XX ID ADX06659 standard; DNA; 1726 BP.  
 XX  
 XX AC ADX06659;  
 XX  
 XX XX  
 XX 21-APR-2005 (first entry)  
 XX  
 XX Cyclin-dependent kinase modulation biomarker DNA SEQ ID NO 1224.  
 XX  
 XX cytosstatic; cyclin-dependent kinase; cdk; biomarker; gene; ds.  
 XX

XX OS Homo sapiens.  
 XX PN WO2005012875-A2.  
 XX PD 10-FEB-2005.  
 XX 29-JUL-2004; 2004WO-US024424.  
 XX PF 29-JUL-2003; 2003US-0490890P.  
 XX PR (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 XX PA  
 XX PI Li M, Rupnow BA, Webster KR, Jackson DG, Wong TW;  
 XX WPI; 2005-163068/17.  
 XX DR P-PSDB; ADX06660.  
 XX PR  
 XX PT Biomarkers useful for predicting or determining the response of a mammal  
 to a cancer treatment comprising administration of a modulator of cyclin-  
 dependent kinase activity.  
 XX PS Claim 5; SEQ ID NO 1224; 141pp; English.  
 XX CC This invention describes a novel method of predicting or determining  
 whether a mammal will respond or is responding to an anti-cancer agent  
 that modulates cyclin-dependent kinase (cdk) activity. The method  
 comprises measuring the level of one or more biomarkers selected from  
 2774 biomarkers given in the specification (nucleotide sequence SEQ ID  
 NO:1246 (Genbank EST W28729) is especially preferred). The method of the  
 invention is utilized in a kit for determining or predicting whether  
 patient would be susceptible or resistant to treatment by an agent  
 modulating cdk activity. The invention also describes a method for  
 utilizing individualized genetic profiles for treating diseases and  
 disorders based on patient's response and molecular level, specialized  
 microarrays comprising the biomarkers described, antibodies directed  
 against the biomarkers and a cell culture model to identify biomarkers.  
 The cdk modulator is preferably N-5-[(5-(1,1-dimethylethyl)-2-oxazolylmethylthio]-2-thiazolyl-4-piperidine carboxamide, 0.5-L-  
 tartaric acid salt. Note: The sequence data for this patent did not form  
 part of the printed specification, but was obtained in electronic format  
 directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences. This  
 sequence encodes a biomarker used in the method of the invention.  
 XX SQ Sequence 1726 BP; 411 A; 543 C; 481 G; 291 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 1.02e-140 Length: 1726  
 Score: 2097.00 Matches: 395  
 Percent Similarity: 99.7% Conservative: 0  
 Best Local Similarity: 99.7% Mismatches: 1  
 Query Match: 99.6% Indels: 0  
 DB: 14 Gaps: 0

US-10-469-221-2 (1-396) x ADX06659 (1-1726)

Qy 1 SerGlnGlyGlnSerProValProPheProAlaProAlaProProGlnProPro 20  
 Db 391 TCCAGGGCCAGAGCCCGCGGTGCGGTTCCTCCCGCCCGCGCGCGCGCGCGCC 450  
 Qy 21 ThrProAlaLeuProHisProAlaGlnProProProProProGlnGlnPhePro 40  
 Db 451 ACCCTCGCCCTGCGCGACCCCGCGCGAGCGCGCGCGCGCGCGCGCGCGCG 510  
 Qy 41 GlnPheHisValLysSerglyLeuGlnIleLysLysAsnAlaIleLeuAspTyrLys 60  
 Db 511 CAGTTCACGCTCAAGTCCGGCCTCGAGATCAAGAAGAACGCGCATCATCGATCAAG 570  
 Qy 61 ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLys 80  
 Db 571 GTCCACGACGAGGTCCTGGGGCTGGGCATCAACGGCAAGATTTTGCAGATCTTCAAC 630  
 Qy '81 ArgThrGlnGluLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaArgGlu 100

Db 631 AGGACCCAGAGAAATTCGCCCTCAAAATGCTTCAGACTGCCCAAGGCCCGAGGGAG 690  
 Qy ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr 120  
 Db 691 GTGGAGCTGCACTGGCGGGCCTCCCAAGTGCCTCGATCGATCGATCGATCGATCG 750  
 Qy GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly 140  
 Db 751 GAGAACTCTGTACGCGAGGAGGAAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTG 810  
 Qy GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer 160  
 Db 811 GAACTCTTTAGCCCAATCCAGGATCAGGAGACCGAGCATTCACAGAAAGAGAGCATCC 870  
 Qy GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis 180  
 Db 871 GAAATCATGAAGAGCATCGGTGAGGCATCCAGTATCTGCATTCATCAATCAATTCGCCAT 930  
 Qy ArgAspValLysProGluAsnLeuTyrThrSerLysArgProAsnAlaIleLeuLys 200  
 Db 931 CGGGATGTCAAGCCTGAGAAATCTTTATACACTCCAAAAGGCCCAACGCCCATCTCTGAAA 990  
 Qy LeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCys 220  
 Db 991 CTCACCTGACTTTGGCTTTGCCAAGGAAACACCCAGGCACAACTCTTTGACCACCTCTGT 1050  
 Qy TyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys 240  
 Db 1051 TATACACCGTACTATGTGGCTCCAGAAAGTCTGGGTCCAGAGAAAGTATGACAAAGTCTGT 1110  
 Qy AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProProPheTyr 260  
 Db 1111 GACATGTGGTCCCTGGGTGCATCATGTATCATCTGCTGTGGGTATTCCTCCCTCTCTAC 1170  
 Qy SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr 280  
 Db 1171 TCCAAACACCGCCTTCCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGCCAGTAT 1230  
 Qy GluPheProAsnProGluTrpSerGluValSerGluValSerGluValLysMetLeuIleArgAsn 300  
 Db 1231 GAATTTCCCAACCCAGAAATGGTCCAGAAATGATCAGAGAGAGTGAAGATGCTCATTCGGAAT 1290  
 Qy LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTyr 320  
 Db 1291 CTGCTGAAACACAGACCCCAAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 1350  
 Qy IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGlu 340  
 Db 1351 ATCATGCAATCAACAAAGGTCCCTCAAAACCCCACTGCACACCAAGCGGTCTCTGAAGAG 1410  
 Qy AspLysGluArgTrpGluAspValLysGluGluMetThrSerAlaLeuAlaThrMetArg 360  
 Db 1411 GACAAGGAGCGGTGGGAGGATGTCAAGAGGAGGATGACCAAGTGCCTTGGCCCAATCGCC 1470  
 Qy ValAspTyrGluGlnIleLysIleLysLysIleGluAspAlaSerAsnProLeuLeuLeu 380  
 Db 1471 GTTGACTACGACGATCAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 1530  
 Qy LysArgArgLysLysAlaArgAlaLeuGluAlaAlaAlaLeuAlaHis 396  
 Db 1531 AAGAGCGGAAGAAAGCTCGGGCCCTGGAGGCTCGGGCTCGGGCTCGGGCTCGGGCTCG 1578

RESULT 6  
 ABK84657  
 ID ABK84657 standard; cDNA; 1336 BP.  
 XX  
 AC ABK84657;  
 XX  
 DT 14-AUG-2002 (first entry)  
 XX  
 DE Human cDNA differentially expressed in granulocytic cells #1228.  
 XX

KW Human; ss; granulocytic cell; DNA chip; bacterial infection;  
 KW viral infection; parasitic infection; protozoal infection;  
 KW fungal infection; sterile inflammatory disease; psoriasis;  
 KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;  
 KW cardiac reperfusion injury; renal reperfusion injury; ARDS;  
 KW adult respiratory distress syndrome; inflammatory bowel disease;  
 KW Crohn's disease; ulcerative colitis; periodontal disease;  
 KW granulocyte activation; chronic inflammation; allergy.

XX Homo sapiens.

XX WO200228999-A2.

XX PD 11-APR-2002.

XX PF 03-OCT-2001; 2001WO-US030821.

XX PR 03-OCT-2000; 2000US-0237189P.

XX PA (GENE-) GENE LOGIC INC.

XX PI Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;

XX DR WPI; 2002-435328/46.

XX PT Detecting granulocyte activation by detecting differential expression of  
 genes associated with granulocyte activation, which serves as diagnostic  
 markers that is useful for monitoring disease states and drug toxicity.

XX PS Claim 1; SEQ ID NO 1228; 114pp; English.

XX The invention relates to detecting (M1) granulocyte (GC) activation  
 (GCA), by detecting the level of expression of gene(s) (Gs) identified by  
 DNA chip analysis as given in the specification, and comparing the  
 expression level to an expression level in an unactivated GC, where  
 differential expression of Gs is indicative of GCA. Also included are  
 modulating (M2) GA by contacting GC with an agent that alters the  
 expression of at least one gene in Gs; (2) screening (M3) for an agent  
 capable of modulating GCA or an inflammation (especially chronic) in a  
 tissue, an allergic response in a subject, exposure of a subject to a  
 pathogen or sterile inflammatory disease using the gene expression  
 profile; (3) detecting (M4) an inflammation (especially chronic) in a  
 tissue, an allergic response in a subject, exposure of a subject to a  
 pathogen or sterile inflammatory disease, by detecting the level of  
 expression in a sample of the tissue of gene(s) from Gs, where the level  
 of expression of the gene is indicative of inflammation; (4) treating  
 (M5) an inflammation (especially chronic) or in a tissue, an allergic  
 response in a subject, exposure of a subject to a pathogen or sterile  
 inflammatory disease, by contacting a tissue having inflammation with an  
 agent that modulates the expression of gene(s) from Gs in the tissue. M1  
 is useful for detecting GCA; M2 is useful for modulating GA; M3 is useful  
 for screening an agent capable of modulating GCA preferably in an  
 inflammation in a tissue; M4 is useful for detecting an inflammation  
 (especially chronic) in a tissue, an allergic response in a subject,  
 exposure of a subject to a pathogen or sterile inflammatory disease (e.g.  
 psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis,  
 cardiac reperfusion injury, renal reperfusion injury, ARDS, adult  
 respiratory distress syndrome, inflammatory bowel disease, Crohn's  
 disease, ulcerative colitis, periodontal disease; also bacterial  
 infection, viral infection, parasitic infection, protozoal infection,  
 fungal infection and M5 is useful for treating one of the above  
 conditions. The present sequence represents a gene differentially  
 expressed in granulocytes. Note: The sequence data for this patent did  
 not form part of the printed specification, but was obtained in  
 electronic format directly from WIPO at  
 ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 1336 BP; 338 A; 406 C; 340 G; 252 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.75e-139 Length: 1336  
 Score: 2078.00 Matches: 393  
 Percent Similarity: 99.2% Conservative: 0

Best Local Similarity: 99.2% Mismatches: 3  
 Query Match: 98.7% Indels: 0  
 DB: 6 Gaps: 0

US-10-469-221-2 (1-396) x ABK84657 (1-1336)

QY 1 SerGlnGlyGlnSerProProValProPheProAlaProAlaProProGlnProPro 20  
 DB 1 TCCGAGGGCCAGAGCCCGCGGTGCGTTCCTCCCGCCCGCGCGCGCGCGCCCC 60

QY 21 ThrProAlaLeuProHisProProAlaGlnProProProProProGlnGlnPhePro 40  
 DB 61 ACCCTGCTGCTGCGCACCCCGCGCGCAGCGCGCGCGCGCGCGCGCGCGCGCG 120

QY 41 GlnPheHisValLysSerGlyLeuGlnLysValLysValLysValLysValLys 60  
 DB 121 CAGTTCCACGTCAAGTCCGGCTCGAGATCAAGAGAACGCCATCATCTGACTAC 180

QY 61 ValThrSerGlnValLeuGlyLeuGlyLeuGlyLeuGlyLeuGlyLeuGlyLeu 80  
 DB 181 GTCAACGACCGAGGTCTTGGGCTGGGCATCAACGGCAAGTTTTCGAGATCTTCA 240

QY 81 ArgThrGlnGluLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaArgGlu 100  
 DB 241 AGGACCCAGGAGAAATTCGCCCTCAAAATGCTTCAGGACTGCCCAAGGCCG 300

QY 101 ValGluLeuHisTrpArgAlaSerGlnCysProHisValValArgLysValTyr 120  
 DB 301 GTGAGCTGCACCTGGCGGGCTCCAGTGGCCCGACATCGTACGGATCGTGAT 360

QY 121 GluAsnLeuTyrAlaGlyArgLysCysLeuLeuLeuValMetGluCysLeuAspGly 140  
 DB 361 GAGAAATCTGTACGAGGAGGAGAGTGCCTGCTGATTGTCATGGAATGTTTG 420

QY 141 GluLeuPheSerArgLysGlnAspArgGlyAspGlnAlaPheThrGluArgGluA 160  
 DB 421 GAATCTTTAGCCGAATCCAGGATCGAGAGACAGGACATTCACAGAAAGAG 480

QY 161 GluLeuMetLysSerLeuGlyGluAlaLeuGlnTyrLeuHisSerLeuAlaHis 180  
 DB 481 GAAATCATGAAGACATCGGTGAGGCCATTCAGTATCTGCATTCATCAACAT 540

QY 181 ArgAspValLysProGluAsnLeuTyrThrSerLysArgProAsnAlaLeuLys 200  
 DB 541 CGGGATGTAAGCTCGAGATCTTATACACCTCCAAAGGCCCAAGCCCTCTG 600

QY 201 LeuThrAspPheGlyPheAlaLysGluThrThrSerHisSerLeuThrThrPro 220  
 DB 601 CTCACCTACTTGGCTTTGGCAAGGAAACCCAGCCACCAACTCTTTGACCA 660

QY 221 TyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLys 240  
 DB 661 TATACACCGTACTATGTTGGCTCCAGAAAGTCTGGGTCCAGAGAAGTATGA 720

QY 241 AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProPhe 260  
 DB 721 GACATGTTGCTCTGGGTGTCATCATCTGCTGCTGCTGCTGCTGCTGCTGCT 780

QY 261 SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgLysArgMetGly 280  
 DB 781 TCCAAACACCGCCCTTGCCATCTCTCCGGGATGAAGACTCGCATCCGAATGG 840

QY 281 GluPheProAsnProGluTyrSerGluValSerGluGluValLysMetLeuIle 300  
 DB 841 GAATTTCCCAACCCAGAAATGTCAGAAATATCAGAGGAAGTGAAGATGCTCA 900

QY 301 LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHis 320  
 DB 901 CTGCTGAAAACAGAGCCCAACCCAGAGAAATGACCATCACCGAGTTTATGA 960

QY 321 IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeu 340  
 DB 961 ATCATGCAATCAACAAAGTCCCTCAAAACCCCACTGCACACCCAGCCGGGCT 1020





Db	781	TCCAAACACAGCGCCTTGGCATCTCTCCGGGCGATGAAGACTCGCATCCGAATGGGCCAGAT	840
Qy	281	GluPheProAsnProGluTrrpSerGluValSerGluGluVallysMetLeuIleArgAsn	300
Db	841	GAAITTTCCCAACCCAGAAATGGTCAGAAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT	900
Qy	301	LeuLeuIysThrGluPuOrThrGlnArgMetThrIleThrGluPheMetAsnHisProTrrp	320
Db	901	CTGCTGAAAAACAGAGCCACCCAGAGAAATGACCATCACCGAGTTTATGAACCAACCCCTTGG	960
Qy	321	IleMetGlnSerThrIysValProGlnThrProIeuHisThrSerArgValLeuIysGlu	340
Db	961	ATCATGCAATCAACAAAGAGTCCCTCAACCCCCACTGCACACCAAGCGGGTCTCGAAGGAG	1020
Qy	341	AspLysGluArgTrrpGluAspVallysGluGluMetThrSerAlaLeuAlaThrMetArg	360
Db	1021	GACAAGAGCGGTGGAGATGTCAAGAGGAGATGACCAAGTGCTTGGCCCAACATCGCG	1080
Qy	361	ValAspTyrGluGlnIleIleIysIleLysIleGluAspAlaSerAsnProLeuLeuLeu	380
Db	1081	GTTTGACTACGAGCAGATCAAGATAAAAAAGATTGAAGATGCATCCCAACCCCTCTGCTGCTG	1140
Qy	381	LysArgArgIysLysAlaArgAlaLeuGluAlaAlaLeuAlaHis	396
Db	1141	AAGAGGCGGAAGAAAGCTCGGGCCCTGGAGCTCGGCTCTGGGCCAC	1188

CC cell and immunological response gene expression. Note: The present  
CC sequence does not appear in the printed specification but was obtained in  
CC electronic format from the USPTO web site.  
CC ([seqdata.uspto.gov/sequence.html?DocID=200400077003](http://seqdata.uspto.gov/sequence.html?DocID=200400077003)).



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Oy 261 SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr 280
Db 1171 TCCAAACACGCGCTTCCATCTCTCCGGCATGAGACTCGCATCCGATGGCCAGTAT 1230
Oy 281 GluPheProAsnProGluTrpSerGluValSerGluGluValLysMetLeuIleArgAsn 300
Db 1231 GAATTTCCCAACCCAGATGGTCAGAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT 1290
Oy 301 LeuLeuLysThrGluProThrGluArgMetThrIleThrGluPheMetAsnHisProTrp 320
Db 1291 CTGCTGAACACAGAGCCACCCAGAGAATGACCATCACCGAGTTTATGAACACCCCTTGG 1350
Oy 321 IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGlu 340
Db 1351 ATCATGCAATCAACAAAGTCCCTCAAAACCCCACTGCACACAGCCGGTCTCTGAAGGAG 1410
Oy 341 AspLysGluArgTrpGluAspValys----- 349
Db 1411 GACAAGGAGCGGTGGGAGGATGTCAAGGGGTGTCTTTCATGACAAGAACAGCGACCGGCC 1470
Oy 349 ----- 349
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Oy 349 ----- 349
Db 1531 TCTTAGAATCCTTTTATTCCTGGGTCTCTAATGGGACCTTAAAGACCATCTGTTATCAT 1590
Oy 349 ----- 349
Db 1591 CTTCTCATTTTGCAGAGAGAAACTGAGGCCCGAGGGCGGAGGCGAGTCTCTCAAGTGC 1650
Oy 349 ----- 349
Db 1651 ACGCAGCTGTGACTGTGTGGGGGACAGCCGACCCAGGTTTCTGACTCTGTGGCCCAAGT 1710
Oy 349 ----- 349
Db 1711 CTCTTCTCTATCTCTGGGATCACTGGGGGCTCTCAGGGAACAGCAGTGCCATA 1770
Oy 349 ----- 349
Db 1771 GCCAGGCTCTCTGCTGCCAGCGCTGGGGTGAGGCTGCGGTGTGTGAGCGTGACCACTAA 1830
Oy 349 ----- 349
Db 1831 CCAGCCGCTTCTCTCTCTGCTCCACCCCTGCCGCCCTCACCTGCGCTTGTGTCTC 1890
Oy 349 ----- 349
Db 1891 TGTCTCTCAGCTCTCTCTCTGCTGCTCTCTCTACCTGCTCTTGGCTCTCTGTACCC 1950
Oy 350 -----GluGluMetThrSerAlaLeuAlaThrMetArgVal 361
Db 1951 TTCTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2010
Oy 362 AspTyrGluGlnIleLysIleLysLysIleGluAspAlaSerAsnProLeuLeuLys 381
Db 2011 GACTACGAGCAGATCAAGATAAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 2070
Oy 382 ArgArgLysLysAlaArgAlaLeuGluAlaAlaLeuAlaHis 396
Db 2071 AGCGGGAAGAAAGCTCGGCGCTGAGGCTCGGCTCTGCGCCAC 2115
RESULT 10
ACAG2272
ID ACA62272 standard; DNA; 2263 BP.
XX AC
AC ACA62272;
XX AC
DT 11-AUG-2003 (first entry)
XX
```

```
DE Human DNA encoding MAPKAP kinase 2.
KW Human; ds; gene; tyrosine threonine kinase; TTK; cancer; cytostatic;
KW mitotic checkpoint gene; MAPKAP kinase 2.
XX Homo sapiens.
FH Key Location/Qualifiers
FT CDS 379..1491
FT /*tag= a
FT /product= "MAPKAP kinase 2"
PN US2003045491-A1.
XX 06-MAR-2003.
PF 21-FEB-2002; 2002US-00081119.
PR 23-FEB-2001; 2001US-0289813P.
PA (REIN/) REINHARD C.
PA (JEFF/) JEFFERSON A B.
PA (CHAN/) CHAN V W.
XX Reinhard C, Jefferson AB, Chan VW;
XX WPI; 2003-456566/43.
XX P-PSDB; ABU61622.
XX Detecting cancer in a subject, by comparing expression levels of tyrosine
XX threonine kinase polypeptide or polynucleotide in a subject cell and a
XX normal cell, where an increase in the expression level in the test cell
XX is indicative of cancer.
XX Disclosure; Page 59-61; 79pp; English.
XX The invention relates to detecting cancer (other than ovarian cancer) in
XX a subject, comprising comparing the expression levels of tyrosine
XX threonine kinase (TTK, a mitotic checkpoint gene) polypeptide or
XX polynucleotide in a test cell obtained from the subject and in a normal
XX non-cancer cell, where an increase in the expression level of TTK protein
XX or nucleic acid in the test cell compared to that in the normal cell,
XX indicates the presence of cancer other than ovarian cancer. Also included
XX are reducing growth of a cancerous cell (by contacting a cancerous cell
XX with an amount of an agent effective to reduce TTK polypeptide activity
XX in the cell), an assay for identifying a candidate agent that reduces
XX growth of a cancerous cell (comprising: (i) detecting the activity of a
XX TTK polypeptide in the presence of a candidate agent; and (ii) comparing
XX the activity of TTK polypeptide in the presence of a candidate agent
XX relative to TTK polypeptide activity in the absence of the candidate
XX agent), identifying an agent that reduces TTK activity (comprising: (i)
XX contacting a cancerous cell displaying elevated expression of a TTK-
XX encoding polynucleotide with a candidate agent; and (ii) determining the
XX effect of the candidate agent on TTK polypeptide activity) and assessing
XX the prognosis of a cancerous disease other than ovarian cancer in a
XX subject (comprising: (i) detecting expression of TTK -encoding
XX polynucleotide in a test cancer cell of a subject; and (ii) comparing a
XX level of expression of TTK-encoding polynucleotide in the test cancer
XX cell with a level of expression of the polynucleotide in a control non-
XX cancer cell, where the level of expression of TTK in the test cancer cell
XX relative to the level of expression in the control non-cancer cell is
XX indicative of the prognosis of the cancerous disease). The methods are
XX useful for detecting cancer (other than ovarian cancer) in a subject,
XX reducing growth of cancerous cells, identifying a candidate agent that
XX reduces growth of a cancerous cell, identifying an agent that reduces TTK
XX activity and assessing the prognosis of a cancerous disease other than
XX ovarian cancer. The methods are also useful for determining the ability
XX of a subject to respond to a particular therapy e.g. as a basis of
XX rational therapy. The present sequence encodes another protein which is
XX differentially expressed in cancer tissues, in this case human MAPKAP
XX kinase 2
XX Sequence 2263 BP; 496 A; 716 C; 618 G; 433 T; 0 U; 0 Other;
```

Alignment Scores:

Baseline Score:	4.1e-134	Length:	2263
Pred. No.:	Score:	Matches:	396
	Score:	Conservative:	0
	Percent Similarity:	Mismatches:	0
	Best Local Similarity:	Indels:	179
	Query Match:	Gaps:	1
	DB:		9

US-10-469-221-2 (1-396) x ACA62272 (1-2263)

Qy		1	SerGlnGlyGlnSerProProValProPheProAlaProProGlnProPro	20
Db		391	TCCCAGGGCGCAGACGCCGGCTGTCCC	450
Qy		21	ThrProAlaLeuProHisProProAlaGlnProProProProGlnGlnPhePro	40
Db		451	ACCCTTGCCCTTGCAGCACCCCGCGCGAGCGCGCGCGCGCGCATTC	510
Qy		41	GlnPheHisValLysSerGlyLeuGlnIleLysAsnAlaIleLysAspPheTyrLys	60
Db		511	CAGTTCCACGTCAGATCGGCGCTGCAGATCAAGAAGAACGCCATCATCGACTACAAG	570
Qy		61	ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLys	80
Db		571	GTCAACAGCCAGGTCCTGGGCGCTGGGATCAACCGCAAAGTTTTGTCAGATCTTCAACAAG	630
Qy		81	ArgThrGlnGluLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaArgAsgGlu	100
Db		631	AGGACCCAGGAAATTGCGCCTCAAAATGCTTCAGGACTGCCCAAGGCCCGCAGGGAG	690
Qy		101	ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr	120
Db		691	GTGAGCTGCATCGCGGGCTCCAGTAGTCCCGCACATCGTACGGATCGTGGATGTGTAC	750
Qy		121	GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly	140
Db		751	GAGAAATCTGTACGAGGAGGAAGTGCCTGCTGATGTCTATGGAAATGTTTGGACCGTGGA	810
Qy		141	GluLeuPheSerArgIleGlnAspArgLysAspGlnAlaPheThrGluArgGluAlaSer	160
Db		811	GAACTCTTTAGCCGAATCCAGGATCGAGGAGACCAAGCATTCACAGAAAGAGAAGCATCC	870
Qy		161	GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis	180
Db		871	GAATAATCAAGAGCATCGGTGAGGCCATCCAGTATCTGCAATTCAAATCAACATTCGCCAT	930
Qy		181	ArgAspValLysProGluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeuLys	200
Db		931	CGGATGTCAAGCCTGAGAAATCTCTTATACACCTCCAAGAGGCCCAAGCCATCCTGAAA	990
Qy		201	LeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCys	220
Db		991	CTCACTGACTTTGGCTTTGCCAAGGAACCAACAGCAGCCACAACTCTTTGACCACTCCITGT	1050
Qy		221	TyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys	240
Db		1051	TATACCGCTACTATGTGGCTCCAAGAGTGTGGGTCCAGAGAAAGTATGCAAGTCCCTGT	1110
Qy		241	AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProProPheTyr	260
Db		1111	GACATGTGGTCCCTGGGTGTTCATCATGTACATCTCTGTGTGGGTATCCCCCTTCTAC	1170
Qy		261	SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr	280
Db		1171	TCCAACCAACGGCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCAGTAT	1230
Qy		281	GluPheProAsnProGluTrpSerGluValSerGluGluValLysMetLeuIleArgAsn	300
Db		1231	GAATTTCCCAACCCAGAAATGTGTGAAAGTATCAGAGGAAGTGAAGATGTCTATTCGGAA	1290
Qy		301	LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTrp	320

KW peripheral occlusive arterial disease; atherosclerosis;  
 KW thrombotic condition; thromboembolic condition; CNS disorder; human;  
 KW MK2 variant 1; chromosome 1q32; gene; ss.

XX Homo sapiens.

OS Key Location/Qualifiers  
 FT CDS 379..1491  
 FT /\*tag= a  
 FT /product= "MK2 variant 1"

XX WO2004017909-A2.

XX 04-MAR-2004.

XX 21-AUG-2003; 2003WO-US026337.

XX 23-AUG-2002; 2002US-040586P.

XX (BRIM ) BRISTOL-MYERS SQUIBB CO.

XX Wang X, Schieven G, Feuerstein GZ;

XX WPI; 2004-226726/21.

XX P-ESDB; ADM36338.

XX Reducing or treating ischemic injury, comprises administering an  
 XX inhibitor of mitogen-activated protein kinase-activated protein kinase 2  
 XX (MK2) activity or expression.

XX Disclosure; SEQ ID NO 1; 39pp; English.

XX The present invention describes a method for reducing ischaemic injury in  
 CC a mammal, which comprises administering a compound that reduces the  
 CC activity of mitogen-activated protein kinase-activated protein kinase 2  
 CC (MK2) or that inhibits MK2 expression. Also described: (1) identifying a  
 CC compound which inhibits MK2 expression in a cell, or which modulates MK2  
 CC activity; (2) compounds identified by the method above; and (3) treating  
 CC ischaemic injury by administering to a patient a compound above, or an  
 CC MK2 modulator. The compound has vasotropic, cerebroprotective, cardiant,  
 CC hypotensive, antiarteriosclerotic, thrombolytic, neuroprotective,  
 CC cardiovascular, antianginal and antiarrhythmic activities, and can be  
 CC used as an MK2 antagonist. The method is useful reducing or treating  
 CC ischaemic injury, particularly cerebral ischaemia. Compounds identified  
 CC by the method are useful for treating ischaemia. (e.g. ischaemia  
 CC resulting from vascular occlusion, cerebral infarction, stroke, and  
 CC related cerebral vascular diseases), myocardial infarction, coronary  
 CC artery disease, congestive heart failure, cardiac arrhythmias, unstable  
 CC angina, high blood pressure, claudication, peripheral occlusive arterial  
 CC disease, atherosclerosis, thrombotic or thromboembolic conditions, or CNS  
 CC disorders associated with cerebral ischaemia. The present sequence  
 CC encodes the human MK2 variant 1, which is located on chromosome 1q32.

XX SQ Sequence 2263 BP; 496 A; 716 C; 618 G; 433 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4,1e-134 Length: 2263  
 Score: 2006.50 Matches: 396  
 Percent Similarity: 68.9% Conservative: 0  
 Best Local Similarity: 68.9% Mismatches: 179  
 Query Match: 95.3% Indels: 1  
 DB: 12 Gaps: 1

US-10-469-221-2 (1-396) x ADM36337 (1-2263)

Qy 1 SerGlnGlyGlnSerProProValProPheProAlaProAlaProProGlnProPro 20

Db 391 TCCAGGCGCCAGAGCGCGCGGTTCCTCCCGCGCGCGCGCGCGCGCGCGCGCGCC 450

Qy 21 ThrProAlaLeuProHisProProAlaGlnProProProProGlnGlnPhePro 40

Db 451 ACCCTGCTCCGCGACACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 510

Qy 41 GlnPheHisValIysSerGlyLeuGlnIleLysLysAsnAlaIleIleAspAspTyrLys 60  
 Db 511 CAGTTCACGTCAAGTCCGGCTGCAGATCAAGAGAACGCCCATCATCATGACTACAAG 570  
 Qy 61 ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLys 80  
 Db 571 GTCACACGACGAGTCTCTGGGGCTGGGCATCAACGGCAAGTTTTCAGAGATCTTCAACAAG 630  
 Qy 81 ArgThrGlnGluLysPheAlaLeuMetLeuGlnAspCysProLysAlaAaArgGlu 100  
 Db 631 AGGACCCAGAGAGAAATTCGCCCTCAAAATGCTTCAGGACTGCCCAAGGCCCGCAGGAG 690  
 Qy 101 ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr 120  
 Db 691 GTGGAGCTGCACCTGGCGGGCTCCAGTGCCTGCACATCGTACGATCGTGGATGTGTAC 750  
 Qy 121 GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly 140  
 Db 751 GAGAAATCTGTACGCGAGGAGAGTGCCTGTGATTGTCATGGAATGTTTGGACGGTGA 810  
 Qy 141 GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer 160  
 Db 811 GAATCTTTAGCCGAATCCAGGATCGAGGAGACAGGAGATTCACAGAAAGAGAGATCC 870  
 Qy 161 GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis 180  
 Db 871 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCATCAATCAACATTCGCCAT 930  
 Qy 181 ArgAspValLysProGluAsnLeuTyrThrSerLysArgProAsnAlaIleLeuLys 200  
 Db 931 CGGGATGTCAAGCTCGAGAATCTTTATACACCTCCAAAAGGCCCAACGCCATCTCTGAAA 990  
 Qy 201 LeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCys 220  
 Db 991 CTCACTACATTCGCTTGGTTCGAGGAAACACAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1050  
 Qy 221 TyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys 240  
 Db 1051 TATACACCGTACTATGTGGCTCCAGAAAGTGTGGTCCAGAGAAAGTATGACAACTCTGT 1110  
 Qy 241 AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProProPheTyr 260  
 Db 1111 GACATGTGTGTCCTGGGTGTGCATGATGATCATCTGTGTGGGTATTCCTCCCTCTTAC 1170  
 Qy 261 SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr 280  
 Db 1171 TCCAAACCGCGCTTGGCATCTCTCGGGCATGAGAGCTCGCATCCGATGGGCGAGTAT 1230  
 Qy 281 GluPheProAsnProGluTrpSerGluValSerGluGluValLysMetLeuIleArgAsn 300  
 Db 1231 GAATTTCCCAACCCAGAAATGGTCAGAAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT 1290  
 Qy 301 LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTrp 320  
 Db 1291 CTGCTGAAAAACAGAGCCACCCAGAGAAATGACCATCACCATCCAGATTATGAACACCCCTGG 1350  
 Qy 321 IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGlu 340  
 Db 1351 ATCATGCATCAACAAGGTCCCTCAAAACCCACTGCACACCGAGCGCGGTCTCTGAAGGAG 1410  
 Qy 341 AspLysGluArgTrpGluAspValLys----- 349  
 Db 1411 GACAAGGAGCGGTGGGAGGATGTCAAGGGGTGTCTTCATGACAAGAAACAGCGACCGGCC 1470  
 Qy 349 ----- 349  
 Db 1471 ACTTGGCTGACAGGTTGTGAGCAGAGGATTCGTGTCTGTCTGTCCTCAAACTCAGTGTGT 1530  
 Qy 349 ----- 349  
 Db 1531 TCTTAGAATCTTTTATTCCTCGGTCTCTAATGGGACCTTAAAGACCATCTGATCAT 1590  
 Qy 349 ----- 349









PR 21-FEB-2001; 2001US-0271254P.  
 PR 21-FEB-2002; 2002US-00081119.  
 PR 06-FEB-2003; 2003US-00360848.  
 PR 30-OCT-2003; 2003US-00698959.  
 PR 22-JAN-2004; 2004US-00763692.  
 XX  
 PA (CHIR ) CHIRON CORP.  
 XX  
 XX Reinhard C, Jefferson AB, Chan VW, Kaufmann J, Xin H, Kennedy GC;  
 PI Harrowe G, Khoja H, Shyamala V;  
 XX P-PSDB; AEA89440.  
 DR WPI; 2005-457024/46.  
 XX  
 XX New isolated human HX2004-6 polypeptide or isolated VSHK-1 polypeptide,  
 PT useful for diagnosing or treating cancer, where VSHK-1 is also used to  
 PT identify a VSHK-1 receptor ligand.  
 XX  
 XX Disclosure; SEQ ID NO 33; 206pp; English.  
 PS  
 XX The invention relates to human HX2004-6 protein and a seven transmembrane  
 CC receptor protein referred as VSHK-1 useful for diagnosing or treating  
 CC cancer. The invention also relates to a method for reducing the growth of  
 CC a cancerous cell. VSHK-1 is useful for identifying a VSHK-1 receptor  
 CC ligand and to identify a substance which modulates its signal  
 CC transduction activity. The HX2004-6 DNA is useful to detect the presence  
 CC of HX2004-6 in a biological sample (e.g. ductal epithelial cells from  
 CC tissue chosen from pancreas, colon and breast). The invention is useful  
 CC for screening drugs for the treatment of cancer. The present sequence is  
 CC the human mitogen-activated protein kinase-activated protein kinase 2  
 CC (MAPKAPK2) gene. This sequence is differentially expressed in cancer  
 CC cells.  
 XX  
 XX

SQ Sequence 2263 BP; 496 A; 716 C; 618 G; 433 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.: 4.1e-134 Length: 2263  
 Score: 2006.50 Matches: 396  
 Percent Similarity: 68.9% Conservative: 0  
 Best Local Similarity: 58.9% Mismatches: 0  
 Query Match: 95.3% Indels: 179  
 DB: 14 Gaps: 1

US-10-469-221-2 (1-396) x AEA89439 (1-2263)

Qy 1 SerGlnGlyGlnSerProProValProPheProAlaProPheProGlnProPro 20  
 Db 391 TCCAGGGCCAGAGCCCGCGGTGCGGTTCCTCCCGCCCGCGCGCCAGCCCCC 450  
 Qy 21 ThrProAlaLeuProHisProProAlaGlnProProProProGlnGlnPhePro 40  
 Db 451 ACCCTGCGCTGCGCACCCCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCG 510  
 Qy 41 GlnPheHisValLysSerGlyLeuGlnLeuLysLysAsnAlaIleAspAspTyrLys 60  
 Db 511 CAGTTCACGTCAGTCCGGCTCGAGATCAAGAAGAACGCGCATCATCGATGACTACAAG 570  
 Qy 61 ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLys 80  
 Db 571 GTCAACAGCCAGGTTCCTGGGGCTGGGCATCAACGGCAAAAGTTTGCAGATCTTCAACAAG 630  
 Qy 81 ArgThrGlnGluLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaArgGlu 100  
 Db 631 AGGACCCAGGAGAAATTCGCCCTCATAATGCTTCAGAGCTGCCCAAGGCCCGCAGGGAG 690  
 Qy 101 ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr 120  
 Db 691 GTGAGCTGCACTGGCGGCTCCAGTGGCGCGCACATCGTACGATCGTGGATGTGTAC 750  
 Qy 121 GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly 140  
 Db 751 GAGAATCTGTACCGAGGGAGGAAGTGCCTGCTGATTTGTCATGGAATGTTTGGACGGTGA 810

Qy 141 GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer 160  
 Db 811 GAACCTTTTAGCCGAATCCAGGATCGAGGAGACGAGGCATTCACAGAAAGAGAGCATCC 870  
 Qy 161 GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis 180  
 Db 871 GAAATCATGAAGAGCATCGGTGAGGCCATCGATATCTGCATTCATCAATCAACATTCGCCAT 930  
 Qy 181 ArgAspValLysProGluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeuLys 200  
 Db 931 CGGGATGTCAAGCTGAGAATCTCTATACACCTCCAAAGGGCCCAACGCCATCCTGAAA 990  
 Qy 201 LeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCys 220  
 Db 991 CTCACCTGACTTGGCTTGGCCAGGAAACCCAGCCACCAACTCTTTGACCACTCTTGT 1050  
 Qy 221 TyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys 240  
 Db 1051 TATACACCGTACTATGTGGCTCCAGAAAGTGTGGGTCCAGAGAAAGTATGACAAGTCTCTGT 1110  
 Qy 241 AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProProPheTyr 260  
 Db 1111 GACATGGTGGTCCCTGGGTGTCATCATGTACATCTGCTGTGGGTATCCCCCTTCTAC 1170  
 Qy 261 SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr 280  
 Db 1171 TCCAACCCAGCGCTTGGCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 1230  
 Qy 281 GluPheProAsnProGluTrpSerGluValSerGluGluValLysMetLeuIleArgAsn 300  
 Db 1231 GAATTTCCCAACCCAGAAATGTCAGAAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT 1290  
 Qy 301 LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTrp 320  
 Db 1291 CTGCTGAAAACAGAGCCCGCCAGAGAAATGACCATCACCGAGTTTATGAACCCCTTGG 1350  
 Qy 321 IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGlu 340  
 Db 1351 ATCATGCAATCAACAAAGGTCTCTCAAAACCCCACTGCACACCCAGCGGGTCTCTGAAGGAG 1410  
 Qy 341 AspLysGluArgTrpGluAspValLys----- 349  
 Db 1411 GACAAGGAGCGGTGGGAGGATGTCAAGGGGTGTCTTCATGACAAGAACAGCGACCGAGCC 1470  
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 Db 1471 ACTTGGCTGACAGGTTGTGAGCAGAGGATTTCTGTGTTCTCTGTCCTCAAACTCAGTGTGTT 1530  
 Qy 349 ----- 349  
 Db 1531 TCTTAGAATCCTTTTATTTCCTGGGTCTCTAATGGGACCTTAAAGACCATCTGTGTATCAT 1590  
 Qy 349 ----- 349  
 Db 1591 CTTCTCATTTTGCAGAGAGAAACTGAGGCCAGAGCGGAGGAGGAGTCTGTCTCAAGGTC 1650  
 Qy 349 ----- 349  
 Db 1651 ACGAGCTGTGACTGGTGGGGCAGACCGGACCCAGGTTTCTGACTCTCTGGGCCAAGT 1710  
 Qy 349 ----- 349  
 Db 1711 CTCTTCCTCTATCTCGGGGATCACTGGGGGGCTCTCAGGGAACAGCAGCAGTGCATTA 1770  
 Qy 349 ----- 349  
 Db 1771 GCCAGGCTCTCTGTCGCCAGCGTGGGGTGAGGCTGCCGTGTGTGACGCTGGACCACTAA 1830  
 Qy 349 ----- 349  
 Db 1831 CCAGCCCGCTCTTCTCTCTGTGCCACCCCTGCGGCCCTCACCCCTGCCCCTTGTGTCTC 1890  
 Qy 349 ----- 349



Db	1319		GACAAAGCGGTGGGAGATGTCAAGGGGTGTTCTTCATCAAGAAACAGCACCAGGCC	1378
Qy	349	-----	-----	349
Db	1379	ACTTGGCTGACCAGGTTGTGACGAGAGGATTCGTGTTCCTGTCCAAACTCAGTGTGCTGTT	1438	
Qy	349	-----	-----	349
Db	1439	TCTTAGAATCCTTTTATTTCCCTGGGTCTTAATGGGACCTTAAAGACCATCTGGTATCAT	1498	
Qy	349	-----	-----	349
Db	1499	CTTCTCATTTTGACAGAGAGAACTGAGGCCACAGAGCGGAGGCGAGTCTGCTCAAGGTC	1558	
Qy	349	-----	-----	349
Db	1559	ACGCAGCTGGTACTGTTGGGGCAGACCGGACCCAGGTTTCTTGACTCTCTGGCCCAAGT	1618	
Qy	349	-----	-----	349
Db	1619	CTCTTCTCCTATCCTCGGGATCACTGGGGGGCTCTCAGGGAACAGCAGCAGTGCCATA	1678	
Qy	349	-----	-----	349
Db	1679	GCCAGGCTCTGTGTCGCCAGCGCTGGGTGAGGTCGCGTTGTACGCTGGACCACATA	1738	
Qy	349	-----	-----	349
Db	1739	CCAGCCGTCCTTCTCTCTGCTCCCACCCCTGCCGCCCTCACCCCTGCCCTTGTGTCTC	1798	
Qy	349	-----	-----	349
Db	1799	TGCTCTCAGCTCTCTCTTCTGCTGTCTCTCTACCTGTCTTCTGGCTCTCTCTGTACCC	1858	
Qy	350	-----	-----	361
Db	1859	TTCTGTGTGTGCGTGCCTCCAGGAGGAGATGACCGTCCCTTGGCCCAATGCGCGTT	1918	
Qy	362	AspTyrGluGlnIleLysIleLysLysIleGluAspAlaSerAsnProLeuLeuLeuLys	391	
Db	1919	GACTACGAGCAGATCAAGATAAAGATTTGAAGATCATCCAAACCTCTGCTGCTGAAG	1978	
Qy	382	ArgArgLysIysAlaArgAlaLeuGluAlaAlaLeuAlaHis	396	
Db	1979	AGCGGAAGAAAGCTCGGGCCCTGGAGGCTCGGCTCTGSCCCAC	2023	

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 19, 2006, 15:44:17 ; Search time 1565 Seconds  
(without alignments)  
4663.805 Million cell updates/sec

Title: US-10-469-221-2

Perfect score: 2106

Sequence: 1 SQGSPVPFPAPPPQPP.....PLLLKRRKKARALEAAALAH 396

Scoring table: BLOSUM62

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Xgapop 10.0 , Xgapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/abs/ABSSWEB\_spool/US10469221/runat\_19062006\_062607\_1349/app\_query.fasta.1  
-DB=Published Applications NA.Main -QFMT=fastap -SUFFIX=rnpbm -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MTN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pt0 -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=200000000 -HOST=abes03h  
-USER=US10469221@CGN\_1\_1\_1675@runat\_19062006\_062607\_1349 -NCPU=6 -ICPU=3  
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA.Main.\*

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2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09A\_PUBCOMB.seq.\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09B\_PUBCOMB.seq.\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10A\_PUBCOMB.seq.\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10B\_PUBCOMB.seq.\*  
8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*  
9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10D\_PUBCOMB.seq.\*  
10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10E\_PUBCOMB.seq.\*  
11: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10F\_PUBCOMB.seq.\*  
12: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10G\_PUBCOMB.seq.\*  
13: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11A\_PUBCOMB.seq.\*  
14: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11B\_PUBCOMB.seq.\*  
15: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11C\_PUBCOMB.seq.\*  
16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11D\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2106	100.0	1191	8	US-10-469-221-1

2	2106	100.0	1203	8	US-10-469-221-3
3	2097	99.6	1726	8	US-10-645-190-3
4	2078	98.7	1336	8	US-10-641-643-1397
5	2006.5	95.3	2263	6	US-10-081-119-33
6	2006.5	95.3	2263	8	US-10-645-190-1
7	2006.5	95.3	2263	10	US-10-951-389-33
8	2006.5	95.3	2263	10	US-10-951-406-33
9	2006.5	95.3	2263	10	US-10-951-477-33
10	2006.5	95.3	2263	10	US-10-977-087-33
11	2006.5	95.3	3608	10	US-10-887-553A-633
12	1991.5	94.6	2258	3	US-09-964-824A-261
13	1991.5	94.6	2258	7	US-10-305-720-1415
14	1991.5	94.6	2258	10	US-10-843-641A-5564
15	1925.5	91.4	2802	3	US-09-925-300-238
16	1729	82.1	1305	7	US-10-338-411-30
17	1729	82.1	1305	8	US-10-389-640-30
18	1716	81.5	1981	8	US-10-294-027-5
19	1709	81.1	1168	16	US-11-128-061-3380
20	1709	81.1	1168	16	US-11-128-049-3380
21	1391	66.0	2481	7	US-10-305-720-1088
22	1391	66.0	2481	8	US-10-298-354-4
23	1391	66.0	2481	11	US-10-501-035-160
24	1391	66.0	2481	16	US-11-122-323-65
25	1201	57.0	2000	13	US-11-097-143-5863
26	1201	57.0	2025	13	US-11-097-143-29036
C 27	1043	49.5	6276	13	US-11-097-143-5662
C 28	1043	49.5	6276	13	US-11-097-143-29035
29	847	40.2	480	9	US-10-723-860-658
30	847	40.2	480	10	US-10-756-149-685
31	784.5	37.3	2060	10	US-10-770-726-24
32	784.5	37.3	2060	16	US-11-152-366-5
33	784.5	37.3	2066	16	US-11-152-366-6
34	783.5	37.2	1968	8	US-10-717-597-326
35	783.5	37.2	1968	10	US-10-872-645-2
36	717	34.0	600	16	US-11-128-061-7022
37	717	34.0	600	16	US-11-128-049-7022
38	712	33.8	496	3	US-09-918-995-4551
39	698.5	33.2	758	3	US-09-910-943-446
40	666.5	31.6	1669	10	US-10-491-467-55
C 41	622	29.5	477	7	US-10-062-674-280
42	586.5	27.8	483	3	US-09-918-995-23785
43	540	25.6	3061	3	US-09-880-107-2146
44	540	25.6	3206	7	US-10-159-563-155
45	540	25.6	3206	10	US-10-517-328-48

#### ALIGNMENTS

##### RESULT 1

US-10-469-221-1  
; Sequence 1, Application US/10469221  
; Publication No. US20040170995A1  
; GENERAL INFORMATION:  
; APPLICANT: LOGRASSO, PHILIP  
; APPLICANT: LISNOCK, JEAN MARIE  
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING  
; TITLE OF INVENTION: A NOVEL HUMAN SIGNAL TRANSDUCING KINASE-MAFKAP-2: ENCODED  
; TITLE OF INVENTION: PROTEINS, CELLS TRANSFORMED THEREWITH AND USES THEREOF  
; FILE REFERENCE: 20813P  
; CURRENT APPLICATION NUMBER: US/10/469,221  
; CURRENT FILING DATE: 2003-08-27  
; PRIOR APPLICATION NUMBER: PCT/US02/05670  
; PRIOR FILING DATE: 2002-02-25  
; PRIOR APPLICATION NUMBER: 60/272,260  
; PRIOR FILING DATE: 2001-02-28  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1191  
; TYPE: DNA  
; ORGANISM: Human  
US-10-469-221-1

Alignment Scores:

Pred. No.:	1.26e-211	Length:	1199
Score:	2106.00	Matches:	396
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	8	Gaps:	0

US-10-469-221-2 (1-396) x US-10-469-221-1 (1-1191)

[illegible]

## RESULT 2

US-10-469-221-3  
; Sequence 3, Application US/10469221  
; Publication No. US20040170995A1

```

? GENERAL INFORMATION:
? APPLICANT: LOGRASSO, PHILIP
? APPLICANT: HAWKINS, JULIO
? APPLICANT: LISNOCK, JEAN MARIE
? TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING
? TITLE OF INVENTION: A NOVEL HUMAN SIGNAL TRANSDUCING KINASE-MAPKAP-2; ENCODED
? TITLE OF INVENTION: PROTEINS, CELLS TRANSFORMED THEREWITH AND USES THEREOF
? FILE REFERENCE: 28813P
? CURRENT APPLICATION NUMBER: US/10/469,221
? CURRENT FILING DATE: 2003-08-27
? PRIOR APPLICATION NUMBER: PCT/US02/05670
? PRIOR FILING DATE: 2002-02-25
? PRIOR APPLICATION NUMBER: 60/272,260
? PRIOR FILING DATE: 2001-02-28
? NUMBER OF SEQ ID NOS: 4
? SOFTWARE: FastSEQ for Windows Version 4.0
? SEQ ID NO 3
? LENGTH: 1203
? TYPE: DNA
? ORGANISM: Human
? US-10-469-221-3

```

Alignment Scores:

Alignment Scores:			
Pred. No.:	1.28e-211	Length:	1203
Score:	2106.00	Matches:	396
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DR:	8	Gaps:	0

US-10-469-221-2 (1-396) x US-10-469-221-3 (1-1203)

Qy		SerGlnGlyGlnSerProValProPheProAlaProAlaProGlnProPro	20
Dd		TCC CAGGGCAGAGCCCGGTTCCTCCGCCCGCGCGCGCGCGCC	72
Qy		ThrProAlaLeuProHisProAlaGlnProProProGlnGlnPhePro	40
Dd		ACCCCTGCCCTGCCGACCCCGCGCAGCCGCCCGCGCGCGCGTCCCG	132
Qy		GlnPheHisValLysSerGlyLeuGlnIleLysAsnAlaIleAseAspTyrLys	60
Dd		CAGTTCCACGTCAGTCCGGCTGCAGATCAAGAAGACGCCCATCATGACTACAAG	192
Qy		ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLys	80
Dd		GTACCAGCCAGGTCCTGGGGCTGGGCATCAACGCCAAAGTTTTTCAGATCTTCAACAAG	252
Qy		ArgThrGlnGluLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaArgArgGlu	100
Dd		AGCACCCAGGAGAAATCGCCCTCAAATGCTTCAGGACTGCCCAAGCCCGCAGGAG	312

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Qy 101 ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValAtxIleValAspValTyr 120
Db 313 GTGGAGCTGCACCTGGCGGGCTCCAGTCAGTCCGCGACATCGTACGGATCGTGATGTGTAC 372
Qy 121 GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly 140
Db 373 GAGAATCTGTACGAGGAGGAAGTGCCTGTGATTGTTCATGGAATGTTTGGACGGTGA 432
Qy 141 GluLeuPheSerArgIleGluAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer 160
Db 433 GAATCTTTTAGCCGAATCCAGATCGAGGACACAGGCAATTCACAGAAAGAGAGCATCC 492
Qy 161 GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis 180
Db 493 GAAATCATGAAGAGCATCGGTGAGGCCATCAGTATCTGCATTCATCAACATGCCCCAT 552
Qy 181 ArgAspValLysProGluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeuLys 200
Db 553 CGGGATGTCAAGCCTGAGAATCTCTTATACACCTCCAAAAGGCCCAACGCCATCTCGAAA 612
Qy 201 LeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCys 220
Db 613 CTCAGTACTTGGCTTGGCCAGAGAAACCCAGCCACCAATCTCTTGACCACTCCTTGT 672
Qy 221 TyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys 240
Db 673 TATACACGTAATATGTGCTCCAGAGTGTGGTCCAGAGATGATGACAAAGTCTCTGT 732
Qy 241 AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProProPheTyr 260
Db 733 GACATGTGCTCCCTGGGTGTTCATCATGTATCATCTGCTGTGGGTATCCCGCTTCTAC 792
Qy 261 SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr 280
Db 793 TCCAAACACAGCCCTTGGCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 852
Qy 281 GluPheProAsnProGluTrpSerGluValSerGluGluValLysMetLeuIleArgAsn 300
Db 853 GAATTTCCCAACCCAGATGTGTAGAGTATCAGAGNAGTGAAGATGCTCATTCGGAAT 912
Qy 301 LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTrp 320
Db 913 CTGCTGAAACAGAGCCACCAGAGAATGACCATCACCGAGTTTATGAACCAACCTTGG 972
Qy 321 IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGlu 340
Db 973 ATCATGCAATCAACAAAGGTCCCTCAACCCCATGACACACCCAGCCGGGTCTGAAGGAG 1032
Qy 341 AspLysGluArgTrpGluAspValLysGluGluMetThrSerAlaLeuAlaThrMetArg 360
Db 1033 GACAGGAGCGTGGAGGATGTCAAGAGGAGATGACAGTGTCTTGGCCACATCGC 1092
Qy 361 ValAspTyrGluGlnIleLysIleLysIleGluAspAlaSerAsnProLeuLeuLeu 380
Db 1093 GTTGACTACGAGCAGATCAAGATAAAAAAGATTGAAGATGCATCCAACCCCTCTGCTGT 1152
Qy 381 LysArgGlyLysAlaArgAlaLeuGluAlaAlaLeuAlaHis 396
Db 1153 AAGAGCGGAAGAAGCTCGGGCCCTCGAGGCTCGCGCTCGGGCCAC 1200
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## RESULT 3

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US-10-645-190-3
; Sequence 3, Application US/10645190
; Publication No. US20040110710A1
; GENERAL INFORMATION:
; APPLICANT: BRISTOL-MYERS SQUIBB COMPANY
; TITLE OF INVENTION: METHODS FOR PREVENTING ISCHEMIC BRAIN INJURY
; FILE REFERENCE: D0299 NP
; CURRENT APPLICATION NUMBER: US/10/645,190
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: 60/405,586
; PRIOR FILING DATE: 2002-08-23
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; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 1726
; TYPE: DNA
; ORGANISM: Human
US-10-645-190-3
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## Alignment Scores:

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Pred. No.: 1.9e-210 Length: 1726
Score: 2097.00 Matches: 395
Percent Similarity: 99.7% Conservative: 0
Best Local Similarity: 99.7% Mismatches: 1
Query Match: 99.6% Indels: 0
DB: 8 Gaps: 0
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US-10-469-221-2 (1-396) x US-10-645-190-3 (1-1726)

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Qy 1 SerGlnGlyGlnSerProProValProPheProAlaProAlaProProGlnProPro 20
Db 391 TCCAGAGGCCAGAGCCCGCGGTGCGTTCCTCCGCGCCCGCGCGCGCGAGCCCC 450
Qy 21 ThrProAlaLeuProHisProProAlaGlnProProProProGlnGlnPhePro 40
Db 451 ACCCTCGCTGCGCACCCTCCGCGCGCGCGCGCGCGCGCGCGCGCGAGTTCCTCC 510
Qy 41 GlnPheHisValLysSerGlyLeuGlnIleLysLysAsnAlaIleAspAspTyrLys 60
Db 511 CAGTTCACGTCAAGTCCGCGCTGCGATCAAGAGAACGCCATCATCGATGACTACAAG 570
Qy 61 ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLys 80
Db 571 GTCACACCCAGGTCCTCGGGCTGGGCATCAACGGCAAGTTTTCAGATCTTCAACAAG 630
Qy 81 ArgThrGlnGluLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaArgArgGlu 100
Db 631 AGGACCCAGGAGAAATTCGCCCTCAAAATGCTTCAGGACTGCCCAAGGCGCGAGGAG 690
Qy 101 ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr 120
Db 691 GTGGAGCTGCACCTGGCGGGCTCCCGAGTGCCTCCGACATCGTACGGATCTGGATGTGTAC 750
Qy 121 GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly 140
Db 751 GAGAACTGTACCGAGGAGGAAGTGCCTGCTGATTGTCATGGAATGTTTGGACGGTGA 810
Qy 141 GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer 160
Db 811 GAACTCTTTAGCCGAATCCAGGATCGAGGAGACCGAGCATTCACAGAAAGAGAGCATCC 870
Qy 161 GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis 180
Db 871 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCATCAACATGCCCCAT 930
Qy 181 ArgAspValLysProGluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeuLys 200
Db 931 CGGGATGTCAAGCCTGAGAATCTCTTATACACCTCCAAAAGGCCCAACGCCATCTCGAAA 990
Qy 201 LeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCys 220
Db 991 CTCAGTACTTGGCTTGGCCAGAGAAACCCAGCCACCACTCTTTGACCACTCTCTGT 1050
Qy 221 TyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys 240
Db 1051 TATACACGTAATATGTGCTCCAGAGTGTGGTCCAGAGATGATGACAAAGTCTCTGT 1110
Qy 241 AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProProPheTyr 260
Db 1111 GACATGTGCTCCCTGGGTGTTCATCATGTATCATCTGCTGTGGGTATCCCGCTTCTAC 1170
Qy 261 SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr 280
Db 1171 TCCAAACACAGCCCTTGGCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 1230
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Qy 281 GluPheProAsnProGluTrpSerGluValSerGluGluValLysMetLeuIleArgAsn 300  
Db 1231 GAATTTCCCAACCCAGAAATGGTCAGAAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAAT 1290  
Qy 301 LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTyr 320  
Db 1291 CTGCTGAALACAGAGCCACCCAGAGAAATGACCATCACCGAGTTTATGAACCAACCCCTTGG 1350  
Qy 321 IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGlu 340  
Db 1351 ATCATGCAATCAACAAAGGTCCTCAAAACCCACTGCACACCCAGCGGGTCCTGAAGGAG 1410  
Qy 341 AspLysGluArgTrpGluAspValLysGluGluMetThrSerAlaLeuAlaThrMetArg 360  
Db 1411 GACAAGAGCGGTGGGAGGATGTCAAGGAGGAGATGACCAAGTGCCTTGGGCCACAATGCGC 1470  
Qy 361 ValAspTyrGluGlnIleLysIleLysLysIleGluAspAlaSerAsnProLeuLeuLeu 380  
Db 1471 GTTGACTACAGCGCATCAGATATAAAGATTGAAGATGCATCCAAACCCCTCTGCTGCTG 1530  
Qy 381 LysArgArgLysLysAlaArgAlaLeuGluAlaAlaLeuAlaHis 396  
Db 1531 AAGAGGCGGAAGAAAGCTCGGGCCCTCGAGGCTGCGGCTCTGGGCCAC 1578

## RESULT 4

US-10-641-643-1397  
; Sequence 1397, Application US/10641643  
; Publication No. US20040077003A1  
; GENERAL INFORMATION:  
; APPLICANT: Cocks, Benjamin G.  
; Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL  
; GENE EXPRESSION  
; NUMBER OF SEQUENCES: 1508  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/641,643  
; FILING DATE: 14-Aug-2003  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: <Unknown>  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0001 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 1397:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1336 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GENBANK  
; CLONE: 9407074  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1397 :  
US-10-641-643-1397

Alignment Scores: 1.34e-208 Length: 1336  
Pred. No.: 2078.00 Matches: 393  
Percent Similarity: 99.2% Conservative: 0  
Best Local Similarity: 99.2% Mismatches: 3  
Query Match: 98.7% Indels: 0  
DB: 8 Gaps: 0  
US-10-469-221-2 (1-396) x US-10-641-643-1397 (1-1336)  
Qy 1 SerGlnGlyGlnSerProProValProPheProAlaProAlaProProGlnProPro 20  
Db 1 TCCACGGGCGACAGCCCGCGGTGCGTTCCTCCCGCCCGCGCGCGCGAGCCCGCC 60  
Qy 21 ThrProAlaLeuProHisProProAlaGlnProProProProProGlnGlnPhePro 40  
Db 61 ACCCTGCTGCTGCGCACCCCGCGGCGACCGCGCGCGCGCGCGCGCGAGCATTTCCCG 120  
Qy 41 GlnPheHisValLysSerGlyLeuGlnIleLysAsnAlaIleLeuAspTyrLys 60  
Db 121 CAGTTCCACGTCAAGTCCGCGCTGCGAGATCAAGAGAACGCCATCATCGATGACTACAG 180  
Qy 61 ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLys 80  
Db 181 GTCACACCGCAGGTCTCTGGGCTGGGCATCAACGCCAAAGTTTTCAGATCTTCAACAAG 240  
Qy 81 ArgThrGlnLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaArgArgGlu 100  
Db 241 AGGACCCAGAGAAATTCGCCCTCAAAATGCTTCAGGACTGCCCGCCAGGCGCGAGGAG 300  
Qy 101 ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr 120  
Db 301 GTGGAGCTGCACTGGCGGCTCCAGTGCCTCCAGTGCCTCCAGTGCCTCCAGTGCCTCCAG 360  
Qy 121 GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly 140  
Db 361 GAGAACTGTACGACGGAGGAAGTGCCTGCTGATGTCATGTAATGTTTGGACGGTGA 420  
Qy 141 GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer 160  
Db 421 GAATCTCTTTAGCCGAATCCAGGATCCAGGATCCAGGAGACCGAGCATTCACAGAAAGAGATCC 480  
Qy 161 GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis 180  
Db 481 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGATTCATCAATCAATTCGCCAT 540  
Qy 181 ArgAspValLysProGluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeuLys 200  
Db 541 CGGGATGTCAAGCCTCAGAAATCTCTTATACACCTCCAAAAGGCCCAACGCGCATCTCTGAAA 600  
Qy 201 LeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrProCys 220  
Db 601 CTCACCTGACTTTGGCTTTGCCAAGGAAACACACGAGCCCAACTCTTTGACCATCTCTGT 660  
Qy 221 TyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys 240  
Db 661 TATACACCGTACTATGTGGCTCCAGAGTGTCTGGTCCAGAGAAATATGACAAAGTCTCTGT 720  
Qy 241 AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProProPheTyr 260  
Db 721 GACATGTTGCTCTGGGTGTCAATCATCATCTGCTGTGTGGTATCTCCCGCTCTCTAC 780  
Qy 261 SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr 280  
Db 781 TCCAAACCGCGCTTCCCATCTCTCGGGCATGAAGACTCGCATCCGAATGGGCGCATAT 840  
Qy 281 GluPheProAsnProGluTrpSerGluValSerGluGluValLysMetLeuIleArgAsn 300  
Db 841 GAATTTCCCAACCCAGAAATGGTTCAGAAATATCAGAGGAAGTGAAGATGCTCATTCGGAAT 900  
Qy 301 LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTyr 320



```

Db 901 CTGTGTAACACAGAGCCACCCAGAGAATGACCATCCAGGATTTCATGAACACCCCTTGG 960
Qy 321 IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGlu 340
Db 961 ATATGCAATCAACAAAGTTCCTCAACCCACTGCACACAGCCGGTCTCTGAAGGAG 1020
Qy 341 AspLysGluArgTrpGluAspValLysGluMetThrSerAlaLeuAlaThrMetArg 360
Db 1021 GACAAGGAGCGGTGGAGGATGTCAAGGAGGAGATGACCACTGCTTGGCCACCAATGCGC 1080
Qy 361 ValAspTyrGluGlnIleLysIleLysLysLysLysLysLysLysLysLysLysLys 380
Db 1081 GTTGACTACGAGCAGATCAAGATATAAAGATTGAAGATGTCATCCACCCCTCTGCTGCTG 1140
Qy 381 LysArgArgLysLysAlaArgAlaLeuGluAlaAlaLeuAlaHis 396
Db 1141 AAGAGCGGAAGAAGCTCGGCGCTGGAGGCTCGGCTCTGGCCAC 1188

RESULT 5
US-10-081-119-33
; Sequence 33, Application US/10081119
; Publication No: US20030045491A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; APPLICANT: Chan, Vivien W.
; TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic
; TITLE OF INVENTION: Target in Cancer
; FILE REFERENCE: 16932.002
; CURRENT APPLICATION NUMBER: US/10/081.119
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/289,813
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 2263
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (379)...(1491)
US-10-081-119-33

Alignment Scores:
Pred. No.: 1e-200 Length: 2263
Score: 2006.50 Matches: 396
Percent Similarity: 68.9% Conservative: 0
Best Local Similarity: 68.9% Mismatches: 0
Query Match: 95.3% Indels: 179
DB: 6 Gaps: 1

US-10-469-221-2 (1-396) x US-10-081-119-33 (1-2263)

Qy 1 SerGlnGlyGlnSerProValProPheProAlaProAlaProProGlnProPro 20
Db 391 TCCAGGCGCCAGAGCCCGCGTTCCTCCCGCCCGCCCGCCCGCCCGCCCGCCCGCC 450
Qy 21 ThrProAlaLeuProHisProProAlaGlnProProProProProGlnPhePro 40
Db 451 ACCCTGCGCTGCGCGACCCCGCGCGCAGCGCGCGCGCGCGCGCGCGCGCGCGAGT 510
Qy 41 GlnPheHisValLysSerGlyLeuGlnIleLysLysLysLysLysLysLysLysLys 60
Db 511 CAGTTCACGTCAGTCCGGCTCGAGATCAAGAAAGAACGCCATCATCGATGACTACAAG 570
Qy 61 ValThrSerGlnValLeuGlyLysLysLysLysLysLysLysLysLysLysLysLys 80
Db 571 GTCACGACGAGGTCTCTGGGCTGGGCATCAACGCGCAAGTTTTCGAGATCTTCAACAAG 630
Qy 81 ArgThrGlnGluLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaArgGlu 100
Db 631 AGGACCCAGGAGAAATTCGCCCTCAAAATGCTTCAGGACTGCCCCCAAGGCCCGCAGGAG 690

```

```

Qy 101 ValGluLeuHisTrpArgAlaSerGlnCysProHisLysValArgIleValAspValTyr 120
Db 691 GTGGAGCTGACCTGCGCGGGCTCCAGTGCCTGCACATCGATCGGATCGTGTATGTTAC 750
Qy 121 GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly 140
Db 751 GAGAAATCTGTACGAGGAGGAGTGCCTGCTGATTGTCATGGAATGTTTGGACGCTGGA 810
Qy 141 GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer 160
Db 811 GAACCTCTTTAGCCGAATCCAGGATCGAGGAGACAGGCATTCACAGAAAGAGAGCATCC 870
Qy 161 GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis 180
Db 871 GAATCATGAGAGCATCGGTGAGGCATCAGTATCTGCATTCATCAACATTCGCCAT 930
Qy 181 ArgAspValLysProGluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeuLys 200
Db 931 CGGGATGTCAAGCTGAGAATCTTTATACACCTCCAAAAGGCCCAACGCCATCCTCAAA 990
Qy 201 LeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCys 220
Db 991 CTCACCTGACTTGGCTTTGCCAAGGAAACCCAGCCACCAACTCTTTTGACCACTCTTGT 1050
Qy 221 TyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys 240
Db 1051 TATACACCGTACTATGTGGCTCCAGAAAGTCTGGGTCCAGAGAAATATGACAGTCTGT 1110
Qy 241 AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProPheTyr 260
Db 1111 GACATGTGGTCCCTGGGTGTCATCATCTGCTGTGGGTATTCCTCCCTCTCTAC 1170
Qy 261 SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr 280
Db 1171 TCCAACCAAGCGCTTGCATCTCTCGGGCATGAAGACTCGCATCCGAATGGGCGCATAT 1230
Qy 281 GluPheProAsnProGluTrpSerGluValSerGluGluValLysMetLeuIleArgAsn 300
Db 1231 GAATTTCCCAACCCAGAAATGCTCAGAAATATCAGAGAAATGCTCATTCGGAAT 1290
Qy 301 LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTrp 320
Db 1291 CTGCTGAAAACAGAGCCACCCAGAGAAATGACCATCACCGAGTTTATGAACACCCCTTGG 1350
Qy 321 IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGlu 340
Db 1351 ATCATGCAATCAACAAAGGTCCCTCAAAACCCACTGCACACCCAGCCGGGTCTCTGAAGGAG 1410
Qy 341 AspLysGluArgTrpGluAspValLys----- 349
Db 1411 GACAAGGCGGTGGAGGATGTCNAGGGGTGCTTTCATGACAAGAACAGCAGCAGCCAGGCC 1470
Qy 349 ----- 349
Db 1471 ACTTGGCTGACAGGTGTTGAGCAGAGGATTCCTGTGTTCTGTCCTGTCCAAACCTCAGTGTGTT 1530
Qy 349 ----- 349
Db 1531 TCTTAGAATCCTTTTATTCCTCGGTCTCTTAATGGGACCTTAAGAGACCATCTGGTATCAT 1590
Qy 349 ----- 349
Db 1591 CTTCTCATTTTGCAGAAAGAAACTGAGGCCCCAGAGCGCGGAGGCGAGCTGCTCAAGGTC 1650
Qy 349 ----- 349
Db 1651 ACGCAGCTGTGTACTGTTGGGGCAGAGCCGACCCAGAGTTTCTGACTCTCTGGCCCCAAGT 1710
Qy 349 ----- 349
Db 1711 CTCTTCTCTCTCTCTGCGGATCATCTGGGGGGCTCTCAGGGAAACAGCAGCAGTGCCATA 1770

```



```
Qy 349 ----- 349
Db 1771 GCCAGGCTCTCTGCTGCCAGCGCTGGGTGAGGCTGCGTGTGTGACGGTGGACCACTAA 1830
Qy 349 ----- 349
Db 1831 CCAGCCCGTCTTCTCTCTGCTGCCACCCCTGCCGCCCTCACCCCTGCCCTTGTGTCTC 1890
Qy 349 ----- 349
Db 1891 TGTCTCTCAGCTCTCTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1950
Qy 350 -----GluluMetThrSerAlaLeuAlaThrMetArgVal 361
Db 1951 TTCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2010
Qy 362 AsptYrGluGlnIleLysIleLysIleLysIleLysIleLysIleLysIleLysIleLysIle 381
Db 2011 GACTACGAGCAGATCAAGATAAAAGATTGAAGATGCATCCAACCCCTCTGCTGCTGAAG 2070
Qy 382 ArgArgLysLysAlaArgAlaLeuGluAlaAlaLeuAlaHis 396
Db 2071 AGGCGGAAGAAGACTCGGGCCCTGGAGGCTGGGGCTCTGGGCCAC 2115
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## RESULT 7

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US-10-951-389-33
; Sequence 33, Application US/10951389
; Publication No. US20050058627A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; APPLICANT: Chan, Vivien W.
; TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic
; FILE REFERENCE: 16932.002
; CURRENT APPLICATION NUMBER: US/10/951,389
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US/10/081,119
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/289,813
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 2263
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (379) ... (1491)
US-10-951-389-33
```

```
Alignment Scores:
Pred. No.: 1e-200 Length: 2263
Score: 2006.50 Matches: 396
Percent Similarity: 68.9% Conservative: 0
Best Local Similarity: 68.9% Mismatches: 0
Query Match: 95.3% Indels: 179
DB: 10 Gaps: 1
```

US-10-469-221-2 (1-396) x US-10-951-389-33 (1-2263)

```
Qy 1 SerGlnGlyGlnSerProValProPheProAlaProAlaProGlnProPro 20
Db 391 TCCAGGGCCAGAGCCCGCGGTGCGTTCCTCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCG 450
Qy 21 ThrProAlaLeuProHisProProAlaGlnProProProProProGlnGlnPhePro 40
Db 451 ACCCTGCGCTGCGCACCCCGCGCGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 510
Qy 41 GlnPheHisValLysSerGlyLeuGlnIleLysLysAlaIleLysAspTyrLys 60
Db 511 CAGTTCACGTCAGTCCGGCTCGATCAAGATCAAGAAACGCCCATCATCGATGACTACAAG 570
```

```
Qy 61 ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLys 80
Db 571 GTACACCGCCAGGTCCTGGGCTGGGCATCAACGGCAAGTTTTTGCAGATCTTCAACAAG 630
Qy 81 ArgThrGlnGluLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaArgGlu 100
Db 631 AGGACCCAGGAGAAATTCGCCCTCAAAATGCTTCAGGACTGCCCAAGGCCCGCAGGGAG 690
Qy 101 ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr 120
Db 691 GTGAGCTGCACTCGCGGGCTCCAGTGCCTCCAGTGCCTCCAGTGCCTCCAGTGCCTCCAGTGC 750
Qy 121 GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly 140
Db 751 GAGAAATCTGTACGAGGAGGAAGTGCCTGCTGATTGTTCATGGAATGTTTGGACGGTGA 810
Qy 141 GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAsnSer 160
Db 811 GAACCTTTAGCCGAATCCAGGATCGAGGACGAGGCAATTCACAGAAAGAGAGCATCC 870
Qy 161 GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis 180
Db 871 GAAATCATGAAGACATCGGTGAGGCCATCCAGTATCTGCATTCATCAATCAATTCGCCCAT 930
Qy 181 ArgAspValLysProGluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeuLys 200
Db 931 CGGGATGTCAAGCTCGAGAATCTTTATACACCTCCAAAGGCCCAAGCCATCTCTGAAA 990
Qy 201 LeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCys 220
Db 991 CTCACCTGACTTTGGCTTTGCCAAGAAACCAACGAGCCACAACTCTTTGACCACTCCTGT 1050
Qy 221 TyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys 240
Db 1051 TATACACCGTACTATGTGGCTCCAGAAAGTGTGGGTCCAGAGAAAGTATGACAACTCTGT 1110
Qy 241 AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProProPheTyr 260
Db 1111 GACATGTGGTCCCTGGGTGCATCATGTATCATCTGCTGTGGGTATCCCTCTTCTAC 1170
Qy 261 SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr 280
Db 1171 TCCAAACCGCGCTTGCATCTCTCCGGCATGAAGACTCGCATCCGAATGGGCGAGTAT 1230
Qy 281 GluPheProAsnProGluTrpSerGluValSerGluGluValLysMetLeuIleArgAsn 300
Db 1231 GAATTTCCCAACCCAGAAATGGTCAGAAAGTATCAGAGGAAGTGAAGATGCTCAITTCGGA 1290
Qy 301 LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTrp 320
Db 1291 CTGCTGAAAACAGAGCCCAACCCAGAGAAATGACCATCACCGAGTTTATGAACCACTTGG 1350
Qy 321 IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGlu 340
Db 1351 ATCATGCAATCAACAAAGGTCCTCAAAACCCCACTGACACACCGCGGCTCTGAGAGGAG 1410
Qy 341 AspLysGluArgTrpGluAspValLys----- 349
Db 1411 GACAAGGAGCGGTGGGAGGATGCAAGGGGTGCTTCATGACAAGAAACAGCGACCGAGGCC 1470
Qy 349 ----- 349
Db 1471 ACTTGGCTGACAGGTGTGTGAGCAGAGGATTTCTGTGTCTGCTCCAAACTCAGTGTGTT 1530
Qy 349 ----- 349
Db 1531 TCTTAGAATCCTTTTATTCCTGGGTCTCTAATGGGACCTTAAAGACCAATCTGTTATCAT 1590
Qy 349 ----- 349
Db 1591 CTTCTCTATTTTGGAGAGAGAAACTAGAGGCCCAAGAGCGGAGGCGAGTCTGTCTCAAGGTC 1650
```

```
QY 349 ----- 349
Db 1651 ACGCAGTGTGACTGTTGGGGCAGACCGGACCCAGGTTTCTGACTCTCTGGCCCAAGT 1710
QY 349 ----- 349
Db 1711 CTCTTCTCTATCTCTGCGGGATCACTGGGGGGCTCTCAGGAAACAGCAGTGGCCATA 1770
QY 349 ----- 349
Db 1771 GCCAGGCTCTCTGCTGCCAGCGCTGGGGTGAGGCTGCCGTGTGTGACGCTGGACCACTAA 1830
QY 349 ----- 349
Db 1831 CCAGCCCGTCTTCTCTCTGCTCCACCCCTGCGGCCCTCACCCCTGCTCTGTGTCTC 1890
QY 349 ----- 349
Db 1891 TGTCTCTCAGCTCTCTCTGCTGCTCTCTCTACCTGTCTTCTGGGCTCTCTGTGACCC 1950
QY 350 -----GluGluMetThrSerAlaLeuAlaThrMetArgVal 361
Db 1951 TTCTGCTGCTGCGTGCCTCCCGCCAGGAGGAGATGACCACTGCTGCTTGGCCACAATGCGGTT 2010
QY 362 AspTyrGluGlnIleLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 381
Db 2011 GACTACGAGCAGATCAAGATAAAGATTGAAGATGCATCCAACTCTGCTGCTGAAG 2070
QY 382 ArgArgLysLysAlaArgAlaLeuGluAlaAlaLeuAlaHis 396
Db 2071 AGCGGGAAGAAGCTCGGGCCCTGGAGGCTGGGCTCTGGCCAC 2115
```

## RESULT 8

```
US-10-951-406-33
; Sequence 33, Application US/10951406
; Publication No. US20050059630A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; APPLICANT: Chan, Vivien W.
; TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic
; TITLE OF INVENTION: Target in Cancer
; FILE REFERENCE: 16932.002
; CURRENT APPLICATION NUMBER: US/10/951,406
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US/10/081,119
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/289,813
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 2263
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (379) ... (1491)
US-10-951-406-33
```

## Alignment Scores:

```
Pred. No.: 1e-200 Length: 2263
Score: 2006.50 Matches: 396
Percent Similarity: 68.9% Conservative: 0
Best Local Similarity: 68.9% Mismatches: 0
Query Match: 95.3% Indels: 179
DB: 10 Gaps: 1
```

US-10-469-221-2 (1-396) x US-10-951-406-33 (1-2263)

```
QY 1 SerGlnGlyGlnSerProProValProPheProAlaProProProGlnProPro 20
Db 391 TCTCAGGCGCCAGAGCCCGCGTTCCTCCCGCCCGCGCGCGCGCGCGCGCC 450
```

```
QY 21 ThrProAlaLeuProHisProProAlaGlnProProProProGlnGlnPhePro 40
Db 451 ACCCTTGCCTTGCACCCCGCGCGAGCGCGCCCGCGCGCGCGCGCGCGCGCGCG 510
QY 41 GlnPheHisValLysSerGlyLeuGlnIleLysLysAsnAlaIleIleAspTyrLys 60
Db 511 CAGTTCACGTCGAGTCCGCGCTGCAGATCAAGAGAACGCCCATCATCGACTACAAG 570
QY 61 ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLys 80
Db 571 GTCAACAGCAGGCTCTGGGGCTGGGCATCAACGGCAAAAGTTTTCAGATCTTCAACAAG 630
QY 81 ArgThrGlnGluLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaArgArgGlu 100
Db 631 AGACCCAGAGAGAAATTCGCCCTCAAAATGCTTCAGACTTGCCTCCCAAGGCCCGAGGAG 690
QY 101 ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr 120
Db 691 GTGGAGCTGCATGGCGGGCTCCAGTGCCTGCACATCGTACGGATCGTGGATGTGTAC 750
QY 121 GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly 140
Db 751 GAGATCTGTACGACGAGGAGGAGTGCCTGCTGATTGTCATGGAATGTTTGGACGGTGA 810
QY 141 GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer 160
Db 811 GAACTCTTTAGCCGAATCCAGGATCCAGGAGACGAGCATTCACAGAAAGAGAGCATCC 870
QY 161 GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis 180
Db 871 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCATCAACATTCGCCAT 930
QY 181 ArgAspValLysProGluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeuLys 200
Db 931 CGGGATGTCAAGCCTGAGAAATCTTTATACACCTCCAAAAGGCCCAACGCCATCTCTGAAA 990
QY 201 LeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCys 220
Db 991 CTCACTGACTTTGGCTTTGCCAAGGAAACCCAGCCAGCCACACTCTTTGACCATCTCTGT 1050
QY 221 TyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys 240
Db 1051 TATACACCGTACTATGTGGCTCCAGAAAGTGTGGTCCAGAGAAATATGACAAAGTCTGT 1110
QY 241 AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProProPheTyr 260
Db 1111 GACATGTGTCTGCTGGGTGCATCATGTATCATCTGCTGTGGGTATCCCGCTTCTAC 1170
QY 261 SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr 280
Db 1171 TCCAACACCGCTTGCCTTCTCCGGGATGAGACTCGCATCGAATGGCCAGTAT 1230
QY 281 GluPheProAsnProGluTrpSerGluValSerGluGluValLysMetLeuIleArgAsn 300
Db 1231 GAATTTCCCAACCCAGAAATGGTCAGAAATATCAGAGAAAGTGAAGATGCTCAITTCGGAAT 1290
QY 301 LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTrp 320
Db 1291 CTGCTGAAAAACAGAGGCCCAAGAGATGACCATCAGGAGTTTATGAACCCCTTGG 1350
QY 321 IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGlu 340
Db 1351 ATCATGCATCAACAAAGGTCCCTCAAAACCCACTGCACACCGCGGGTCTCTGAAGGAG 1410
QY 341 AspLysGluArgTrpGluAspValLys----- 349
Db 1411 GACAAGGAGCGGTGGGAGGATGTCAAGGGGTGTCTTCATGACAAGAACAGCGACCGGCC 1470
QY 349 ----- 349
Db 1471 ACTTGGTGCACAGGTTGTGAGCAGAGGATTCTGTGTTCTCTGCTCCAAACTCAGTGTGTT 1530
```



```
Qy 341 AsplysGluArgTTPGluAspVallys----- 349
Db 1411 GACAAGGCGGTGGAGGATGTCAGGGGTGTTCTTATGACAAGAACAGCGACGAGGCC 1470
Qy 349 ----- 349
Db 1471 ACTTGGCTGACCAGGTGTGAGCAGAGGATCTGTGTCTCTGTTCCAAACTCAGTGTGTT 1530
Qy 349 ----- 349
Db 1531 TCTTGAATCCTTTATTTCCCTGGGTCTCTAATGGGACCTTAAAGACCATCTGGTATCAT 1590
Qy 349 ----- 349
Db 1591 CTTCTCTATTTTGCAGAGAGAACTAGAGGCCAGAGCGGAGGCGAGCTGTCTCAAGGTC 1650
Qy 349 ----- 349
Db 1651 ACGCAGCTGGTGACTGTTGGGGCAGACCGGACCCAGGTTTCCTGACTCTCTGGCCCAAGT 1710
Qy 349 ----- 349
Db 1711 CTCTTCTCTATCTCTGGGATCACTGGGGGCTCTCAGGGAACAGCAGTGGCCATA 1770
Qy 349 ----- 349
Db 1771 GCCAGGCTCTCTGCTGCCAGCGCTGGGGTGAGGCTGCGGTGTGTCAGGGTGGACCACTAA 1830
Qy 349 ----- 349
Db 1831 CCAGCCCGCTTCTCTCTCTGCTCCACCCCTCGCGGCTCACCCCTGCTGTGTGTC 1890
Qy 349 ----- 349
Db 1891 TGTCTCTACGCTCTCTCTGCTGTCTCTCTACCTGTCTTCTGGGCTCTCTGTATCCC 1950
Qy 350 -----GluGluMetThrSerAlaLeuAlaThrMetArgVal 361
Db 1951 TTCTGTGTGTCGTCGTCGCCAGAGGAGATGACCAAGTGCCTTGGCCACAATGCGGTT 2010
Qy 362 AspTyrGluGlnIleLysIleLysLysIleGluAspAlaSerAsnProLeuLeuLys 381
Db 2011 GACTACGAGCAGATCAAGATAAAAGATTGAAGATGCATCAACCTCTCTGCTCTGAAG 2070
Qy 382 ArgArgLysLysAlaArgAlaLeuGluAlaAlaLeuAlaHis 396
Db 2071 AGCGGAAGAAAGCTCGGGCCCTGGAGGCTGCGGCTCTGCGCCAC 2115

RESULT 10
US-10-977-087-33
; Sequence 33, Application US/10977087
; Publication No. US20050130926A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; APPLICANT: Chan, Vivien W.
; APPLICANT: Kaufmann, Joerg
; APPLICANT: Xin, Hong
; APPLICANT: Kennedy, Giulia C.
; APPLICANT: Khajala, Hamiduddin
; APPLICANT: Shyamala, Venkatakrishna
; TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED IN CANCEROUS CELLS
; TITLE OF INVENTION: AND THEIR METHODS OF USE V
; FILE REFERENCE: 2300-21986
; CURRENT APPLICATION NUMBER: US/10/977,087
; CURRENT FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: 10/081,119
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/271,254
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 10/360,848
; PRIOR FILING DATE: 2003-02-06
; PRIOR APPLICATION NUMBER: 09/570,593
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; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: 60/134,112
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 10/763,692
; PRIOR FILING DATE: 2004-01-22
; PRIOR APPLICATION NUMBER: 09/626,301
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: 60/148,936
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/145,612
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: 10/698,959
; PRIOR FILING DATE: 2003-10-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 2263
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (379) ... (1491)
US-10-977-087-33

Alignment Scores:
Pred. No.: 1e-200 Length: 2263
Score: 2006.50 Matches: 396
Percent Similarity: 68.9% Conservative: 0
Best Local Similarity: 68.9% Mismatches: 0
Query Match: 95.3% Indels: 179
DB: 10 Gaps: 1

US-10-469-221-2 (1-396) x US-10-977-087-33 (1-2263)
Qy 1 SerGlnGlyGlnSerProValProPheProAlaProAlaProProGlnProPro 20
Db 391 TCCAGGGCCAGAGCCCGCGGTGCGTTCCTCCGCCCGCCGCCGCCGCCGCC 450
Qy 21 ThrProAlaLeuProHisProProAlaGlnProProProProProGlnPhePro 40
Db 451 ACCCTGCTGCGCAGCCCGCGGCGAGCCCGCGCGCGCGCGCGCGCGCGCG 510
Qy 41 GlnPheHisValLysSerGlyLeuGlnIleLysLysAsnAlaIleLeuAspTyrLys 60
Db 511 CAGTTCACGTCAAGTCCGCGCTTCAGATCAAGAGAACCCCATCTCGATGACTACAAG 570
Qy 61 ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLys 80
Db 571 GTCAACCCAGGCTCTCTGGGGCTGGGCATCAACGGCAAAAGTTTTCAGATCTTCAACAAG 630
Qy 81 ArgThrGlnGlnLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaArgAtcGlu 100
Db 631 AGGACCCAGGAGAAATTCGCCCTCAAAATGCTTCAGGACTGCCCAAGGCCGAGGAG 690
Qy 101 ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr 120
Db 691 GTGAGCTGCATCTGGCGGGCTCCAGTGCCCGCACATCTGACGGATCTGGATGTGTAC 750
Qy 121 GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly 140
Db 751 GAGAATCTGTACGAGGAGAAAGTCTCTGCTGCTATTGTCATGGAATGTTTGGACGCTGGA 810
Qy 141 GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer 160
Db 811 GAACTCTTTAGCCGAATCCAGGATCCAGGAGAGACAGGCATTCACAGAAAGAGACATCC 870
Qy 161 GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis 180
Db 871 GAAATCATGAAGACATCGTGGGCCATCCAGTATCTGATCTCAATCAATTCATTCGCCAT 930
Qy 181 ArgAspValLysProGluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeuLys 200
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Db 931 CGGGATGTCAGAGCTGAGAACTCTTTATACACCTCCAAAAGGCCCAACGCCCATCTCTGAAA 990
Qy 201 LeuThrAspPheGlyPheAlaValGluThrThrSerHisAsnSerLeuThrThrProCys 220
Db 991 CTCACTGACTTGGCTTTGGCCAGAGAAACCCAGGCCCAACTCTTTTGACCACCTCTTGT 1050
Qy 221 TyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys 240
Db 1051 TATACACGCTACTATGTGGCTCCAGAGTGTGGTCCAGAGAAAGTATGACAAGTCTCTGT 1110
Qy 241 AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProProPheTyr 260
Db 1111 GACATGTGGTCCCTGGGTGTCATCATGTATACATCTCTGTGTGGGTATCCCTCTCTAC 1170
Qy 261 SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr 280
Db 1171 TCCAAACACGCTTGGCATCTCTCCGGCATGAAGACTCCGATCCGAATGGGCAGTAT 1230
Qy 281 GluPheProAsnProGluTrpSerGluValSerGluGluValLysMetLeuIleArgAsn 300
Db 1231 GAATTTCCCAACCCAGAAATGTCAGAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT 1290
Qy 301 LeuLeuLysThrGluProThrGluArgMetThrIleThrGluPheMetAsnHisProTrp 320
Db 1291 CTGCTGAAAACAGAGCCCAACCCAGAGATGACCATCACCGAGTTTATGAACACCCCTTGG 1350
Qy 321 IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGlu 340
Db 1351 ATCATGCATCAAAAGGTCCTCAAAACCCACTGCACACAGCCGGGTCTGAAGAG 1410
Qy 341 AspLysGluArgTrpGluAspValLys----- 349
Db 1411 GACAAGAGCGGTGGAGGATGTCAAGGGGTCTTTCATGACACAGAGCAGCAGGCC 1470
Qy 349 ----- 349
Db 1471 ACTTGGCTGACAGGTTGTGAGCAGAGGATTTCTGTGTTCTGTCTCCAACTCAGTGTGTT 1530
Qy 349 ----- 349
Db 1531 TCTTAGAATCTTTATTCCTCGGTCTCTAATGGGACCTTAAGACCATCTGTATCAT 1590
Qy 349 ----- 349
Db 1591 CTTCTCATTTTGACAGAGAAACTGAGGCCAGAGGGGAGGCGAGTCTGCTCAAGTGC 1650
Qy 349 ----- 349
Db 1651 ACGCAGCTGTGACTGTTGGGGCAGACCGGACCCAGGTTTCTGACTCTCTGGCCCAAGT 1710
Qy 349 ----- 349
Db 1711 CTCTTCTCTATCTCGGGATCACTGGGGGGCTCTCAGGGAAACAGAGCAGTGGCCATA 1770
Qy 349 ----- 349
Db 1771 GCCAGGCTCTCTGCTGCCAGCGGTGGGGTGAGGCTGCGGTGTGTCAGGTGGACCACTAA 1830
Qy 349 ----- 349
Db 1831 CCAGCCCGTCTTCTCTCTGCTCCCAACCCCTGCGGCCCTCACCCCTGCTGTGTCTC 1890
Qy 349 ----- 349
Db 1891 TGTCTCTACGTCTCTCTCTGCTGTCTCTCTACCTGTCTTCTGGCTCTCTCTGTACCC 1950
Qy 350 ----- GluGluMetThrSerAlaLeuAlaThrMetArgVal 361
Db 1951 TTCCTGTGTGCTGCGTCCCGCAGGAGGAGATGACCATGTCCTTGGCCACAAATGCGCGTT 2010
Qy 362 AspTyrGluGlnIleLysIleLysLysIleGluAspAlaSerAsnProLeuLeuLys 381
Db 2011 GACTACGAGCAGATCAAGATAAAAAAGATTGAAGATGCATCCAAACCCCTCTGCTCTGAAG 2070
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Qy 382 ArgArgLysLysAlaArgAlaLeuGluAlaAlaAlaLeuAlaHis 396
Db 2071 AGCGGAAGAAGAGCTCGGGCCCTGGAGGCTCGGCTCTGGCCAC 2115
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## RESULT 11

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US-10-887-553A-633
; Sequence 633, Application US/10887553A
; Publication No. US20050085436A1
; GENERAL INFORMATION:
; APPLICANT: Garza, Dan
; APPLICANT: Li, Hao
; TITLE OF INVENTION: Method to treat conditions associated
; with insulin signalling dysregulation
; FILE REFERENCE: 4-33262
; CURRENT APPLICATION NUMBER: US/10/887,553A
; CURRENT FILING DATE: 2004-07-08
; PRIOR APPLICATION NUMBER: 60/485,883
; PRIOR FILING DATE: 2003-08-07
; NUMBER OF SEQ ID NOS: 1208
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 633
; LENGTH: 3608
; TYPE: DNA
; ORGANISM: human
US-10-887-553A-633
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Alignment Scores:
Pred. No.: 1,93e-200 Length: 3608
Score: 2006.50 Matches: 396
Percent Similarity: 68.9% Conservative: 0
Best Local Similarity: 68.9% Mismatches: 0
Query Match: 95.3% Indels: 179
DB: 10 Gaps: 1
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US-10-469-221-2 (1-396) x US-10-887-553A-633 (1-3608)

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Qy 1 SerGlnGlyGlnSerProProValProPheProAlaProAlaProProGlnProPro 20
Db 299 TCCAGGGCCAGAGCCCGCGGTGCGCTCCCGCCCGCGCGCGCGCGCGCGCGCG 358
Qy 21 ThrProAlaLeuProHisProProAlaGlnProProProProGlnGlnPhePro 40
Db 359 ACCCTGCTGCGCGACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 418
Qy 41 GluPheHisValLysSerGlyLeuGlnIleLysLysAsnAlaIleAspAspTyrLys 60
Db 419 CAGTTCACGTCAAGTCCGGCTTCAGATCAAGAAGAACGCCATCATCGATGACTACAAG 478
Qy 61 ValThrSerGlnValLeuGlyValLeuGlyValLeuGlyValLeuGlyValLeuGly 80
Db 479 GTACACAGCCAGGTCTCTGGGGCTGGGCATCAACGGCAAGTTTTCAGATCTTCAACAG 538
Qy 81 ArgThrGlnGlyLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaArgGlu 100
Db 539 AGGACCCAGGAGAAATTCGCCCTCAAAATGCTTTCAGGACTGCGCCCAAGGCGCGAG 598
Qy 101 ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr 120
Db 599 GTGAGCTGCACGTGGGGGCTCTCCAGTGGCCGACATCGATCGGATCGTGGATGTGTAC 658
Qy 121 GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly 140
Db 659 GAGAACTGTACCGAGGAGGAAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 718
Qy 141 GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer 160
Db 719 GAATCTTTTACCGCAATCCAGGATCGAGGAGACAGGCAATTCACAGAAAGAGCAATCC 778
Qy 161 GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis 180
Db 779 GAAATCAATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCATCAATCAATTCGCCAT 838
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Qy 181 ArgAspValLysProGluAunLeuLeuTyThrSerLysArgProAsnAlaIleLeuLys 200  
Db CGGATGTCAGCGCTGAGAATCTCTTATACACCTCCAAAGAGGCCAACGCGCATCTCTGAAA 898  
Qy 201 LeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCys 220  
Db CTCACTGACTTTGGCTTTGGCAGGAACACACAGCCACCACTCTTTGACCACTCTCTTGT 958  
Qy 221 TyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys 240  
Db TATACACCGTACTATGTGGCTCCAGAAAGTGCTGGTCCAGAGAAGTATGACAAAGTCTCTGT 1018  
Qy 241 AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProProPheTyr 260  
Db GACATGTGGTCCCTGGGTGTCATCATGTACATCTGTGTGGGTATCCCCCTTCTAC 1078  
Qy 261 SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr 280  
Db TCCAACCGCCCTTGCATCTCTCCGGGATGAGACTCGCATCCGAATGGGCCAGTAT 1138  
Qy 281 GluPheProAsnProGluTrpSerGluValSerGluValLysMetLeuIleArgAsn 300  
Db GAATTTCCCAACCCAGAAATGTCAGAAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAAT 1198  
Qy 301 LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTyr 320  
Db CTGCTGAAACAGAGCCACCCAGAGAATGACCATCACCGAGTTTATGAACCAACCCCTGG 1258  
Qy 321 IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGlu 340  
Db ATCATGCAATCAACAAAGTCCCTCAAAACCCACTGCACACCCAGCCGGTCTCTGAAGGAG 1318  
Qy 341 AspLysGluArgTrpGluAspValLys----- 349  
Db GACAAGGAGCGGTGGGAGGATGTCAAGGGGTGTTCTTATGACAAGAACAGCGACCGGCC 1378  
Qy 349 ----- 349  
Db ACTTGGCTGACCAAGTTGTGAGCAGAGATTTCTGTGTCTCTGTCACAAACTCAGTGTGTT 1438  
Qy 349 ----- 349  
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Qy 349 ----- 349  
Db CTTCTCATTTTGACAGAGAAACTGAGGCCAGAGGGCGAGGCGAGTCTGTCTCAAGGTC 1558  
Qy 349 ----- 349  
Db ACGCAGTGTGTACTGTTGGGGCAGACCGGACCCAGGTTTCTGACTCTCTGGCCCAAGT 1618  
Qy 349 ----- 349  
Db CTCTTCTCTCATCTCTGGGGATCACTGGGGGGTCTCAGGGAACAGCAGAGTGCCATA 1678  
Qy 349 ----- 349  
Db GCCAGGCTCTCTGCTGCCAGCGTGGGGTGAGGCTGCCGTTGTGAGCGTGGACCACTAA 1738  
Qy 349 ----- 349  
Db CCAGCCCGTCTTCTCTCTGCTCCACCCCTGCGGCCCTCACCCCTGCCCTTGTGTCTC 1798  
Qy 349 ----- 349  
Db TGTCTCTCAGCTCTCTCTGCTGTCTCTCTACCTGTCTTCTGGCTCTCTCTGTACCC 1858  
Qy 350 ----- GluGluMetThrSerAlaLeuAlaThrMetArgVal 361  
Db TTCCTGGTGTGTCGCGTCCAGAGAGATGACCAAGTGCCTTTGGCCCAATGCGCGTT 1918  
Qy 362 AspTyrGluGlnIleLysIleLysLysIleGluAspAlaSerAsnProLeuLeuLeuLys 381

Db 1919 GACTACGACAGATCAAGATAAAAAAGATTGAAGATGCATCCAAACCTCTGTGCTGAAG 1978  
Qy 382 ArgArgLysLysAlaArgAlaLeuGluAlaAlaAlaLeuAlaHis 396  
Db AGGCGGAAGAAAGCTCGGGCCCTGGAGGCTCGGGCTCTGGCCAC 2023  
RESULT 12  
US-09-964-824A-261  
; Sequence 261, Application US/09964824A  
; Patent No. US20020102531A1  
; GENERAL INFORMATION:  
; APPLICANT: Horriagan, Stephen  
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu  
; FILE OF INVENTION: Sets  
; FILE REFERENCE: 689290-73  
; CURRENT APPLICATION NUMBER: US/09/964,824A  
; PRIOR FILING DATE: 2001-09-27  
; PRIOR APPLICATION NUMBER: US/60/236,033  
; PRIOR FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: US/60/236,032  
; PRIOR FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: US/60/236,028  
; PRIOR FILING DATE: 2000-09-28  
; NUMBER OF SEQ ID NOS: 583  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 261  
; LENGTH: 2258  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-964-824A-261  
Alignment Scores:  
Pred. No.: 3,83e-199 Length: 2258  
Score: 1991.50 Matches: 396  
Percent Similarity: 69.0% Conservative: 0  
Best Local Similarity: 69.0% Mismatches: 0  
Query Match: 94.6% Indels: 178  
DB: 3 Gaps: 1  
US-10-469-221-2 (1-396) x US-09-964-824A-261 (1-2258)  
Qy 1 SerGlnGlyGlnSerProValProPheProAlaProAlaProProGlnProPro 20  
Db TCCAGGGCCAGAGCCGCCGCGTTCCTCCCGCCGCCGCCGCCGCCGCCGCCGCC 450  
Qy 21 ThrProAlaLeuProHisProProAlaGlnProProProProProGlnPhePro 40  
Db ACCCTGCTGCTGCGCACCCCGCGCGCAGCGCGCGCGCGCGCGCGCGCGCGCG 510  
Qy 41 GlnPheHisValLysSerGlyLeuGlnIleLysLysAsnAlaIleLeuAspTyrLys 60  
Db CAGTTCACGTCAGTCCGCGCTGCGCATCAAGAAAGCCCATCATCGATGACTACAAG 570  
Qy 61 ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLys 80  
Db GTACACAGCCAGGTCTCTGGGGCTGGGCATCAAGCGCAAGTTTTCAGATCTTCAACAG 630  
Qy 81 ArgThrGlnLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaArgArgLys 100  
Db AGGACCCAGGAGAAATTCGCCCTCAAAATGCTTTCAGGACTGCCCGCCAGGCGCGAG 690  
Qy 101 ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr 120  
Db GTGAGCTGCTGCTGGGGGCTCCCGAGTGGCCGACATCGTAGGATCGTGGATGTGTAC 750  
Qy 121 GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly 140  
Db GAGAACTGTACCGAGGAGGAAGTGCCTGCTGATTGTCATGGAATGTTTGGACGCTGA 810  
Qy 141 GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer 160  
Db GAACTCTTTAGCCGAATCCAGGATCGAGGAGACCGAGCATTTCAGAAAGAGAGCATCC 870



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Qy 161 GluileMetLysSerIleGlyAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis 180
Db 871 GAAATCATGAGAGCATCGGTGAGGCCATCAGTATCTGCATTCAATCAACATGGCCCAT 930
Qy 181 ArgAspValLysProGluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeuLys 200
Db 931 CGGGATGTCAGAGCCTCAGAAATCTCTTATACACCTCCAAAAGGCCCAACGCCCATCCTGAAA 990
Qy 201 LeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCys 220
Db 991 CTCAGTACTTGGCTTGGCCCAAGAAACCCAGCCACCACTCTTTGACCACCTCCTTGT 1050
Qy 221 TyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys 240
Db 1051 TATACACCGTACTATGTGGCTCCAGAGTGTGGTCCAGAGAGATGATGACAACTCCTGT 1110
Qy 241 AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProProPheTyr 260
Db 1111 GACATGTGGTCCCTGGGTGTCTATCATGTATCATCTCTGTGTGGGTATCCCCCTTCTAC 1170
Qy 261 SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGluTyr 280
Db 1171 TCCAAACACGCGCTTGGCATCTCTCCGGGCATGAGACTCGCATCCGAATGGGCAGTAT 1230
Qy 281 GluPheProAsnProGluTrpSerGluValSerGluGluValLysMetLeuIleArgAsn 300
Db 1231 GAAATTTCCCAACCCAGAAATGTCTAGAGATATCAGAGNAGTGAAGATGCTCATTTCCGAAT 1290
Qy 301 LeuLeuLysThrGluProThrGluArgMetThrIleThrGluPheMetAsnHisProTrp 320
Db 1291 CTGCTGAAACACAGAGCCACCAGAGATGATACCATCACCGAGTTTATGAACACCCCTTGG 1350
Qy 321 IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGlu 340
Db 1351 ATCATGCAATCAACAAAGGTCCCTCAACCCCACTGCACACAGCCGGGTCTTGAAGAG 1410
Qy 341 AspLysGluArgTrpGluAspValLys 349
Db 1411 GACAGAGGCGGTGGAGGATGTCAAGGGTGTCTTATGACAGAAACAGGACCGCC 1470
Qy 349 349
Db 1471 ACTTGGCTGACCAAGTGTGAGCAGAGATTTCTGTGTCTGTCTCCAACTCAGTGTCTT 1530
Qy 349 349
Db 1531 TCTTAGAATCCTTTTATTCCTGGGTCTCTAATGGGACCTTAAAGACCATCTGGTATCAT 1590
Qy 349 349
Db 1591 CTTCTCATTTTGACAGAGAAACTGAGGCCAGAGCCGAGGGGAGGTCGTCTCAAGGTC 1650
Qy 349 349
Db 1651 ACGCAGCTGGTGACTGTGGGGCAGACCGGACCCAGGTTTCTGTACTCTGTGGCCCAAGT 1710
Qy 349 349
Db 1711 CTCTTCTCCTATCTCTGGGGATCACTGGGGGGGCTCTCAGGGAACAGACGAGTGCATA 1770
Qy 349 349
Db 1771 GCCAGGCTCTCTGCTGCCACCGCTGGGGTGAGGCTGCCGTTGTTCAGGGTGGACCACTAA 1830
Qy 349 349
Db 1831 CCAGCCGCTCTCTCTCTCTGCTCCACCCCTGCCGCTCACCTGCCCTTGTGTCTGTCTG 1890
Qy 349 349
Db 1891 TCTCTCACTGTCTCTCTGTGTCTCTCTACTGTCTTCTTGTGGCTCTCTCTGTACCCCTTCT 1950
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Qy 350 -----GluMetThrSerAlaLeuAlaThrMetArgValAspTyr 363
Db 1951 GGTGCTCCGCTGCCCCCAGGAGGAGATGACCAAGTGCCTTGGCCACATGCGCGTTGACTA 2010
Qy 363 rGluGlnIleLysIleLysIleGluAspAlaSerAsnProLeuLeuLeuLysArgAr 383
Db 2011 CGAGCAGATCAAGATAAAAGATTGAAGATGATCCAAACCTCTGCTGCTGAAGAGCG 2070
Qy 383 gLyLysAlaArgAlaLeuGluAlaAlaAlaLeuAlaHis 396
Db 2071 GAAGAAAGCTCGGGCCCTGGAGGCTCGGCTCTGGCCAC 2110

RESULT 13
US-10-305-720-1415
; Sequence 1415, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Sellhamer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO 1415
; LENGTH: 2258
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank ID No. US20040010136A1 g530089
US-10-305-720-1415

Alignment Scores:
Pred. No.: 3,83e-199 Length: 2258
Score: 1991.50 Matches: 396
Percent Similarity: 69.0% Conservative: 0
Best Local Similarity: 69.0% Mismatches: 0
Query Match: 94.6% Indels: 178
DB: 7 Gaps: 1

US-10-469-221-2 (1-396) x US-10-305-720-1415 (1-2258)

Qy 1 SerGlnGlyGlnSerProValProPheProAlaProAlaProGlnProPro 20
Db 391 TCCACAGGCGCAGAGCCCGCGGTGCGGTTCCTCCCGCCCGCGCGCGCGCGCGCGCGCG 450
Qy 21 ThrProAlaLeuProHisProProAlaGlnProProProProProProGlnPhePro 40
Db 451 ACCCTGCTGCTGCGCACCCCGCGCGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 510
Qy 41 GlnPheHisValLysSerGlyLeuGlnIleLysLysAsnAlaIleLeuAspTyrLys 60
Db 511 CAGTTCACCTCAAGTCCGCGCTGCAGATCAAGAAGAACGCCATCATCGATGATCAAG 570
Qy 61 ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLys 80
Db 571 GTACACAGCAGGATCTCTGGGGCTGGGCATCAACGGCAAGTTTTCAGAGATCTTCAACAG 630
Qy 81 ArgThrGlnGlyLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaArgArgGlu 100
Db 631 AGACCCAGGAGAAATTCGCCCTCAAAATGCTTCAGGACTGCCCAAGGCCCGCAGGAG 690
Qy 101 ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr 120
Db 691 GTGAGCTGCACTGGGGGCTCCCAAGTGCCTCCAGTGCCTCCAGTGCCTGATGATGTATC 750
Qy 121 GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly 140
Db 751 GAGAACTGTACGAGGAGGAGAGTGCCTGCTGATTTGTAAGAAATTTTGGAGCGGTGA 810
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QY 141 GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer 160
Db |||||
811 GAACCTCTTTAGCGGAATCCAGGATCGAGGAGACGAGCATTCACAGAAAGAGAGCATCC 870
QY 161 GluLeuMetLysSerIleGlyGluAlaIleGlnTyrlleuHisSerIleAsnIleAlaHis 180
Db |||||
871 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTAICTGCATTCATCAATCAACATTCGCCAT 930
QY 181 ArgAspValLysProGluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeuLys 200
Db |||||
931 CGGGATGTCAGGCTGAGATCTCTTATACACCTCCAAAGAGGCCAACGCCATCTCTGAAA 990
QY 201 LeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCys 220
Db |||||
991 CTCACCTGACTTTGGCTTTGGCAGGAACACCCAGCCACCAACTCTTTGACCACTCTCTGT 1050
QY 221 TyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys 240
Db |||||
1051 TATACACCGTACTATGTGGCTCAGAAAGTGTGGTCCAGAGAGTAATGACAAAGTCTGT 1110
QY 241 AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProProPheTyr 260
Db |||||
1111 GACATGTGGTCCCTGGGTGCATCATGTACATCTGTCTGTGGTATCCCTCCCTTCTAC 1170
QY 261 SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr 280
Db |||||
1171 TCCAAACACCGCCTTGCATCTCTCCGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 1230
QY 281 GluPheProAsnProGluTyrSerGluValSerGluGluValLysMetLeuIleArgAsn 300
Db |||||
1231 GAATTTCCCAACCCAGAAATGTCAGAAATATCAGAGAAATGAAGATGCTCATTCGGAAT 1290
QY 301 LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTrp 320
Db |||||
1291 CTGCTGAAACACAGAGCCACCCAGAGAAATGACCATCACCGAGTTTATGAACCACTCTGG 1350
QY 321 IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGlu 340
Db |||||
1351 ATCATGCAATCAACAAAGGTCCCTCAAACCCCATCTGACACCCAGCCGCGGTCTCTGAAGGAG 1410
QY 341 AspLysGluArgTyrGluAspValLys----- 349
Db |||||
1411 GACAAAGGCGGTGGGAGGATGTCAAGGGTGTCCTTATGACAAAGACACGACCGACCGCC 1470
QY 349 ----- 349
Db |||||
1471 ACTTGGCTGACAGGTTGTGACGAGAGATTCTGTGTTCTGTCTCAAACCTCAGTGTGTT 1530
QY 349 ----- 349
Db |||||
1531 TCTTAGAATCCTTTATTCCCTGGGTCTCTAATGGGACCTTAAAGACCATCTGGTATCAT 1590
QY 349 ----- 349
Db |||||
1591 CTTCATTTTGCAGAGAAACTGAGGCCACGAGCGGGGCGGCGAGTCTGCTCAAGGTC 1650
QY 349 ----- 349
Db |||||
1651 ACGCAGCTGGTGAAGTGTGGGGCAGACCGGACCCAGGTTTCTGTACTCTCTGGCCCCAAGT 1710
QY 349 ----- 349
Db |||||
1711 CTCTTCCTCTATCTCTGGGATCATCTGGGGGGCTCTCAGGGAACACGACGAGTGCCATA 1770
QY 349 ----- 349
Db |||||
1771 GCCAGGCTCTCTGCTGCCACGCGTGGGTGAGGCTGCGGTGTGTCAGCGTGGACCACTAA 1830
QY 349 ----- 349
Db |||||
1831 CCAGCCCGTCTTCTCTCTCTGCTCCACCCCTGCCGCTCACCTGCCCCCTTTGTTGTCTGT 1890
QY 349 ----- 349
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Db 1891 TCTCTCACTGTCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1950
QY 350 -----GluGluMetThrSerAlaLeuAlaThrMetArgValAspTyr 363
Db |||||
1951 GGTGTGCGGTGCCCGCCAGGAGGAGATGACAGTGCCTTGGCCACAAATGCGGTTCACATA 2010
QY 363 rGluGlnIleLysIleLysLysIleGluAspAlaSerAsnProLeuLeuLeuLysArgAr 383
Db |||||
2011 CGAGCAGATCAAGATAAAAAAGATTGAAGATGCATCCAAACCTCTCTCTCTCTGAAGAGCG 2070
QY 383 GlyLysAlaArqAlaLeuGluAlaAlaAlaLeuAlaHis 396
Db |||||
2071 GAAGAAAGCTCGGGCCCTGGAGCTCGGCTCTGGCCAC 2110

RESULT 14
US-10-843-641A-5564
; Sequence 5564, Application US/10843641A
; Publication No. US20050064454A1
; GENERAL INFORMATION:
; APPLICANT: Avalon Pharmaceuticals, Inc.
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; FILE OF INVENTION: Signature Gene Sets
; FILE REFERENCE: 689290-189
; CURRENT APPLICATION NUMBER: US/10/843,641A
; CURRENT FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: US/09/873,367
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US/09/954,531
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,436
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,832
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/964,824
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/09/967,768
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/09/968,007
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,347
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,708
; PRIOR FILING DATE: 2001-10-03
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 8447
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5564
; LENGTH: 2258
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-843-641A-5564

Alignment Scores:
Pred. No.: 3,83e-199 Length: 2258
Score: 1991.50 Matches: 396
Percent Similarity: 69.0% Conservative: 0
Best Local Similarity: 69.0% Mismatches: 0
Query Match: 94.6% Indels: 178
DB: 10 Gaps: 1

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Qy	41	GlnPheHisValLysSerGlyLeuGlnIleLysLysAsnAlaIleIleAspAspTyrLys	60
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Qy	61	ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLys	80
Db	571	GTCACCAAGCCAGGTCCTGGGGCTGGGCATCAACCGCAAGTTTTGCAAGATCTTCAACAAG	630
Qy	81	ArgThrGlnGluLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaArgArgGlu	100
Db	631	AGGACCCAGGAGAAATTCCGCCCTCAAAATGCTTCAGGACTGCCCCAAAGGCCGAGGAG	690
Qy	101	ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr	120
Db	691	GTGAGAGCTGCATCTGGCGGGCTCCAGTGGCCCGCACATCGTACGGATCGTGGATGTGTAC	750
Qy	121	GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly	140
Db	751	GAGAAATCTGTACGAGGAGGAGAGTGCTCTGTAATGTTCATGGAAATGTTTGGACGGTGA	810
Qy	141	GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer	160
Db	811	GAACCTTTAGCCGAATCCAGGATCGAGGAGACCAGGCATTCACAGAAAGAGAAGCATCC	870
Qy	161	GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis	180
Db	871	GAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCATCAATCAACATTGCCCAT	930
Qy	181	ArgAspValLysProGluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeuLys	200
Db	931	CGGGATGTCAAGCCTCGAATCTCTTATACACCTCCAAAGAGGCCAACAGGCATCCTGAAA	990
Qy	201	LeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCys	220
Db	991	CTCACTGACCTTGGCTTTGCCAAGAAACCAACAGCCACCACTCTTTGACCACTCCTCTGT	1050
Qy	221	TyrThrProTyrTyrValAlaIaProGluValLeuGlyProGluLysTyrAspLysSerCys	240
Db	1051	TATACACGCTACTATGTGGCTCCAGAAAGTGTGGGGTCAGAGAAGTATGACAAAGTCCTGT	1110
Qy	241	AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProProPheTyr	260
Db	1111	GACATGTGGTCCCTGGGTGTCATCATGTACATCTCTGTGTGGGTATCCCCCTTCTAC	1170
Qy	261	SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr	280
Db	1171	TCCAAACCAAGCCCTTGCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT	1230
Qy	281	GluPheProAsnProGluTrpSerGluValSerGluGluValLysMetLeuIleArgAsn	300
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Qy	301	LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTrp	320
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Qy	341	AspLysGluArgTrpGluAspValLys-----	349
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; Sequence 238, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben,
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 238
; LENGTH: 2802
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (613)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (1800)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-300-238

Alignment Scores:
Pred. No.: 4,84e-192 Length: 2802
Score: 1925.50 Matches: 376
Percent Similarity: 94.7% Conservative: 0
Best Local Similarity: 94.7% Mismatches: 3
Query Match: 91.4% Indels: 19
DB: 3 Gaps: 1

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US-10-469-221-2 (1-396) x US-09-925-300-238 (1-2802)

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Qy 41 GlnPheHisValLysSerGlyLeuGlnIleLysLysAsnAlaIleLeuAspTyrLys 60
Db 109 CAGTTCACGTCAGTCCGCGCTGCAGATCAAGAGAACCCCATCATCGATGACTACAAG 168
Qy 61 ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLys 80
Db 169 GTCACCAGCCAGGTCTCTGGGGCTGGGCATCAAGCGCAAAAGTTTTCAGAGATCTTCAACAAG 228
Qy 81 ArgThrGlnGluLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaArgGlu 100
Db 229 AGGACCCAGGAGAAATTCGCCCTCAAAATGCTTCAGGACTGCCCCCAAGGCCCGCAG-GAG 287
Qy 101 ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr 120
Db 288 GTGGAGCTGCACGTGGCGGGCTCCCACTGCCCGCACATCGTACGGATCGTGGATGTGTAC 347
Qy 121 GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly 140
Db 348 GAGAAATCTGTACGCAGGAGAGAGTGCCTGCTGATTGTCATGGAATGTTTGGACCGGTGGA 407
Qy 141 GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer 160
Db 408 GAACTCTTTAGCGAAATCCAGGATTCAGAGAGACAGGCAATTCACAGAAAGAGAGCATCC 467
Qy 161 GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis 180
Db 468 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCAATCAACATTGCCCAT 527
Qy 181 ArgAspValLysProGluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeuLys 200
Db 528 CGGGATGTCAAGCCTGAGAAATCTCTTATACACCTCCAAAAGGCCCAACGCCCATCCTGAAA 587
Qy 201 LeuThrAspPheGlyPheAlaLys-GluThrThrSerHisAsnSerLeuThrThrProCy 220
Db 588 CTCACTGACTTTGGCTTTGCGAGNAAACCCAGGCCACAACCTCTTTGACCACTCCTTG 647
Qy 220 sTyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCy 240
Db 648 TTATACACCGTACTATGTGGCTCCAGAAAGTGTGGGTCCAGAGAAAGTATGACAAAGTCCTG 707
Qy 240 sAspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProProPheTy 260
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Qy 380 uLysArgArgLysLysAlaArgAlaLeuGluAlaAlaLeuAlaHis 396
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Search completed: June 19, 2006, 16:19:02  
Job time : 1593 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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Run on: June 19, 2006, 15:47:29 ; Search time 42 Seconds  
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Title: US-10-469-221-2

Perfect score: 2106

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Ygapop 10.0 , Ygapext 0.5  
Delgap 6.0 , Fgapext 7.0  
Delgap 6.0 , Delxext 7.0

Searched: 290227 seqs, 117694381 residues

Total number of hits satisfying chosen parameters: 580454

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database :

Published Applications NA New:  
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2: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US06\_NEW\_PUB.seq:  
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8: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US60\_NEW\_PUB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	1391	66.0	2509	6	US-10-505-928-626
4	799	37.9	574	6	US-10-488-619-2938
5	522	24.8	1740	7	US-11-242-505A-40
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10	479	22.7	3982	6	US-10-505-928-350
11	466	22.1	4098	7	US-11-293-697-891
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16	448	21.3	2127	6	US-10-449-902-26500
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21	429.5	20.4	2252	6	US-10-449-902-16109
22	428	20.3	1545	7	US-11-217-529-372
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#### ALIGNMENTS

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; Sequence 2, Application US/11273567  
; Publication No. US20060115453A1  
; GENERAL INFORMATION:  
; APPLICANT: Yaffe, Michael B.  
; APPLICANT: Manke, Isaac A.  
; APPLICANT: Reinhardt, Hans Christian  
; APPLICANT: Lim, Daniel  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING CELLULAR PROLIFERATIVE DISEASES  
; FILE REFERENCE: 01997/557002  
; CURRENT APPLICATION NUMBER: US/11/273,567  
; CURRENT FILING DATE: 2005-11-14  
; PRIOR APPLICATION NUMBER: 60/627,352  
; PRIOR FILING DATE: 2004-11-12  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: Patentin version 3.3  
; SEQ ID NO 2  
; LENGTH: 3071  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-273-567-2

Alignment Scores:  
Pred. No.: 1.24e-144  
Score: 2106.00  
Percent Similarity: 100.0%  
Best Local Similarity: 100.0%  
Query Match: 100.0%  
Indels: 0  
Gaps: 0  
DB: 0

US-10-469-221-2 (1-396) x US-11-273-567-2 (1-3071)

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Db 359 ACCCTGCTCCGCGACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 418
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RESULT 2
US-11-273-567-1
; Sequence 1, Application US/11273567
; Publication No. US20060115453A1
; GENERAL INFORMATION:
; APPLICANT: Yaffe, Michael B.
; APPLICANT: Manke, Isaac A.
; APPLICANT: Reinhardt, Hans Christian
; APPLICANT: Lim, Daniel
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING CELLULAR PROLIFERATIVE
; FILE REFERENCE: 01997/557002
; CURRENT APPLICATION NUMBER: US/11/273,567
; CURRENT FILING DATE: 2005-11-14
; PRIOR APPLICATION NUMBER: 60/627,352
; PRIOR FILING DATE: 2004-11-12
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 3608
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-273-567-1
Alignment Scores:
Pred. No.: 2,55e-137 Length: 3608
Score: 2006.50 Matches: 396
Percent Similarity: 68.9% Conservative: 0
Best Local Similarity: 68.9% Mismatches: 0
Query Match: 95.3% Indels: 179
DB: 7 Gaps: 1
US-10-469-221-2 (1-396) x US-11-273-567-1 (1-3608)
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Db 299 TCCAGGGCCAGAGCCCGCGGTGCGGTCCCGCCCGCGCGCGCGCGCGCC 358
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Db 419 CAGTTCACGTCAAGTCGCGCTGCAGATCAAGAAGAACGCCATCATCGATGACTACAAG 478
Qy 61 ValThrSerGlnValLeuGlyLeuGlyLeuGlyLeuGlyValLeuGlnLysPheAsnLys 80
Db 479 GTCAACAGCCAGGTCTCTGGGGCTGGGCATCAACGGCAAGTTTGCAGATCTTCAACAAG 538
Qy 81 ArgThrGlnGluLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaArgGlu 100
Db 539 AGGACCCAGGAGAAATTCGGCCCTCAAAATGCTTCAGGACTGCCCAAGGCCCGCAGGGAG 598
Qy 101 ValGluLeuHisTrpArgAlaSerGlnCysProHisLeuValArgLysValAspValTyr 120
Db 599 GTGGAGCTGCACGTGGCGGCTCCAGTGCCTGCAGATCGTACGATCGTGGATGTGTAC 658
Qy 121 GluAsnLeuTyrAlaGlyArgLysCysLeuLeuLeuValMetGluCysLeuAspGlyGly 140
Db 659 GAGAATCTGTACGCGAGGAGAAATGCTGCTGATGTCATGGAATTTTGGACGGTGA 718
Qy 141 GluLeuPheSerArgLysGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer 160
Db 719 GAATCTTTAGCGAATTCAGGATCGAGGAGACGAGGCATTCACAGAAAGAGAGCATCC 778
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Qy 161 GluileMetLysSerIleGlyAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis 180
Db 779 GAATCATGAGAGCATCGGTAGGCCATCCAGTATCTGCATTCATCAATCAATGCGCAT 838
Qy 181 ArgAspValLysProGluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeuLys 200
Db 839 CGGATGTCAGGCTGAGATCTCTTATACACCTCCAAAGGCCCAAGCCATCTCTGAAA 898
Qy 201 LeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCys 220
Db 899 CTCACCTGACTTGGCTTGGCAAGGAAACCCAGCCAGCCACACTCTTTGACCACTCTGT 958
Qy 221 TyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys 240
Db 959 TATACACCGTACTATGTGGCTCCAGAGAGTGTGGTCCAGAGAGATATGACAAAGTCTGT 1018
Qy 241 AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProProPheTyr 260
Db 1019 GACATGTGGTCCCTGGGTGTCTATCATGTATCATCTGCTGTGGGTATCCCCCTTCTAC 1078
Qy 261 SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr 280
Db 1079 TCCAAACACGCGCTGGCATCTCTCCGGGCGATGAGACTCGCATCCGAAATGGGCCAGTAT 1138
Qy 281 GluPheProAsnProGluTyrTrpSerGluValSerGluGluValLysMetLeuIleArgAsn 300
Db 1139 GAATTTCCCAACCCAGAAATGTCAGAGATATCAGAGAGATGAGATGCTCATTCGGAAT 1198
Qy 301 LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTrp 320
Db 1199 CTGCTGAAAACAGAGGCCACCCAGAGAAATGACCATCACCGAGTTTATGAACCAACCTTGG 1258
Qy 321 IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGlu 340
Db 1259 ATCATGCAATCAACAAGGTCCCTCAAAACCCCACTGCACACCAAGCGGGTCTGGAAGGAG 1318
Qy 341 AspLysGluArgTyrGluAspValLys----- 349
Db 1319 GACAAAGAGCGGTGGGAGGATGTCAAGGGTGTCTTCATGACAGAACAGGACGACGCC 1378
Qy 349 ----- 349
Db 1379 ACTTGGCTGACAGGTGTGAGCAGAGAGATTCTGTGTTCTGTCTCCAAACTCAGTGTGTT 1438
Qy 349 ----- 349
Db 1439 TCTTAGAATCCTTTTATTCCTCGGTCTCTAAATGGGACCTTAAAGACCATCTGGTATCAT 1498
Qy 349 ----- 349
Db 1499 CTTCCTATTGTCAGAGAGAAACTGAGGCCAGAGCGGGGAGGCGAGTCTGCTCAAGGTC 1558
Qy 349 ----- 349
Db 1559 ACGCAGCTGGTGAAGTGTGGGCGAGACCGGACCCAGGTTTCTGACTCTCTGGGCCCAAGT 1618
Qy 349 ----- 349
Db 1619 CTCTTCCTCTATCTCGGGATCATCTGGGGGGTCTTCAGGGAAACAGCAGAGTGCCATA 1678
Qy 349 ----- 349
Db 1679 GCCAGGCTCTCTGTCGCCAGCGTGGGGTGAGGCTGCCGTTGTTCAGCGTGGACCACTAA 1738
Qy 349 ----- 349
Db 1739 CCAGCCGCTCTCTCTCTCTGCTCCACCCCTGCCGCCCTCACCCCTGCTTGTGTCTC 1798
Qy 349 ----- 349
Db 1799 TGTCTCACGCTCTCTCTCTGCTGTCTCTCTTACCTGTCTCTTGGTCTCTCTGTACCC 1858
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Qy 350 -----GluGluMetThrSerAlaLeuAlaThrMetArgVal 361
Db 1859 TTCTGTGTGTCGCGTCCCGCCAGGAGAGATGACCAAGTGCCTTGGCCACAATGCGGTT 1918
Qy 362 AspTyrGluGlnIleLysIleLysIleGluAspAlaSerAsnProLeuLeuLys 381
Db 1919 GACTACGAGCAGATCAAGATATAAAGATTGAAGATGCATCCCAACCCCTCTGCTCTGAAG 1978
Qy 382 ArgArgLysLysAlaAlaGlnLeuGluAlaAlaLeuAlaHis 396
Db 1979 AGCGGAAGAAAGCTCGGGCCCTGGAGGCTGCGGCTCTGGCCCCAC 2023
RESULT 3
US-10-505-928-626
; Sequence 626 Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 626
; LENGTH: 2509
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928-626
Alignment Scores:
Pred. No.: 9,18e-93 Length: 2509
Score: 1391.00 Matches: 265
Percent Similarity: 80.2% Conservative: 50
Best Local Similarity: 67.4% Mismatches: 56
Query Match: 66.0% Indels: 22
DB: Gaps: 3
US-10-469-221-2 (1-396) x US-10-505-928-626 (1-2509)
Qy 1 SerGlnGlySerProProValProPheProAlaProAlaProProGlnProPro 20
Db 134 GCAGAGGAGCAGGGGGCCCTGTGCC-----CCGCCAGTTGCACCGGC 178
Qy 21 ThrProAlaLeuProHisProProAlaGlnProProProProGlnGlnPhePro 40
Db 179 GGACCCCGCTTGGCGGTGCTCCGGGGGGCGCGGGAGGCC----- 220
Qy 41 GlnPheHisValLysSerGlyLeuGlnIleLysLysAsnAlaIleAspTyrLys 60
Db 221 -----AAGAGTACGAGTACCGACGACGACTACAG 250
Qy 61 ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLys 80
Db 251 TTGTCCAAAGCAGGTGCTGGGCTGGGTGTGAACGGCAAGTGTGTGAGTGTCTTCATCGG 310
Qy 81 ArgThrGlnGluLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaArgArgGlu 100
Db 311 CGCACTGGACAGAAAGTGTGCCCTGAAAGCTCCTGTATGACAGCCCCAAGGCCGCGAGAG 370
Qy 101 ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr 120
Db 371 GTAGACCATCATCTGGCAGGCTTCTGGCGGCCCCCATATTGTCTGCATCTCTGATGTAT 430
Qy 121 GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly 140
Db 431 GAGACATGCACCATGCAAGCGCTGTCTCTCATCATCATCATGGAATGCAAGAGGTGT 490
Qy 141 GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer 160
Db 491 GAGTTGTTACGAGGATTACGAGCGGTGGCGCAGCGCTTTCATCTGAGAGAAAGTGC 550
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Qy	161	GlulileMetLysSerlleGlyGluAlaIleGlnTyrLeuHisSerlleAenlleAlaHis	180
Db	551	GAGATAATGCGGATATTGGCACTGCCATCCAGTTTCTGCACAGCCATACATATGCCAC	610
Qy	181	ArgAspVallysProGluAenLeuTyrThrSerLysArgProAenAlaIleLeuLys	200
Db	611	CGAGATGTAAGGCTGAAACCTTACTCTACACATCTTAAGAGAAAGCAGCGTGCTTAAG	670
Qy	201	LeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCys	220
Db	671	CTCACCGATTGGCTTTGCTTGTCTAAGGAGACCACC--CAAAATGCCCTGCACACACCCCTGC	727
Qy	221	TyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys	240
Db	728	TATACTCCCTTATTATGTGGGCCCTCTAGGTCTCGGTCCAGAGAAGTATGACAAAGTCATGT	787
Qy	241	AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProProPheTyr	260
Db	788	GACATGTGGTCCCTGGGTGTACATCATCTCTTGTGGCTTCCCAACCCTTCTAC	847
Qy	261	SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr	280
Db	848	TCCAACACGGGCCAGGCCATCTCCCGGGGATGAAGAGGAGGATTCGCCTGGGCCAGTAC	907
Qy	281	GlupheProAsnProGluTrpSerGluValSerGluGluVallysMetLeuIleArgAsn	300
Db	908	GGCTTCCCCAATCTGTAGTGGTCTCAGAACTCTCTGAGGATGCCAAGCAGCTGTATCCGCCCTC	967
Qy	301	LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTyr	320
Db	968	CTGTTGAAGACAGACCCACAGAGAGGCTGACCATCTCAGTTTCATGAACCAACCCCTGG	1027
Qy	321	IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGlu	340
Db	1028	ATCAACCAATCGATGGTGTAGTGCACACAGACCCCACTCCACACGGCCGCGAGTGTGCAGGAG	1087
Qy	341	AspLysGluArgTrpGluAspValLysGluGluMetThrSerAlaLeuAlaThrMetArg	360
Db	1088	GACAAAGACCACTGGGACGAAGTCAAGGAGGAGATGACCACTGCTTGGCCACTATGCGG	1147
Qy	361	ValAspTyrGluGlnIleLysIleLysLysIleGluAspAlaSerAsnProLeuLeuLeu	380
Db	1148	GTAGACTACACCAAGTGAAGATCAAGGACTCTAAGACCTCTAACACCGGCTCTCTCAAC	1207
Qy	381	LysArgArgLysLysAlaArgAlaLeuGluAlaAla 393	
Db	1208	AAGAGGAGAAAAAAGCAGGCAGGCAGCTCTCTGCTCTCA	1246
RESULT 4			
US-10-488-619-2938			
; Sequence 2938, Application US/10488619			
; Publication No. US20060099578A1			
; GENERAL INFORMATION:			
; APPLICANT: Greenlee, Winner and Sullivan, P.C.			
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations			
; FILE REFERENCE: 98-01 WO			
; CURRENT APPLICATION NUMBER: US/10/488,619			
; NUMBER OF SEQ ID NOS: 3040			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 2938			
; LENGTH: 574			
; TYPE: DNA			
; ORGANISM: Mus musculus			
US-10-488-619-2938			
Alignment Scores:			
Pred. No.:	1.76e-50	Length:	574
Score:	799.00	Matches:	152
Percent Similarity:	99.4%	Conservative:	2
Best Local Similarity:	98.1%	Mismatches:	1

Query Match:	37.9%	Indels:	0
DB:	6	Gaps:	0
US-10-469-221-2 (1-396) x US-10-488-619-2938 (1-574)			
Qy	242	MetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProProPheTyrSer	261
Db	1	ATGTGTCTCTGGGTGTCTATCATGTATATTTTGTGTGGGTATCCCCCTTCTATTCC	60
Qy	262	AsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyrGlu	281
Db	61	AATCAGCGCTTGGCCATCTCTCGGGCATGAAGACTCGTATTCCAATGGCCAGTATGAA	120
Qy	282	PheProAsnProGluTrpSerGluValSerGluGluVallysMetLeuIleArgAsnLeu	301
Db	121	TTTCTCTAACCCCGATTTGGTCAGAAATGATCAGAAATTCATGAACCAACCCCTGGATC	180
Qy	302	LeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTyrIle	321
Db	181	CTAAAAACAGAGCCCAACCCAGAGATGACCATCAGAAATTCATGAACCAACCCCTGGATC	240
Qy	322	MetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGluAsp	341
Db	241	ATGCAATCTACGAAGTCCCTCAGACTCCACCTGCACACAGCCGCTGTCTCTGAAGAGGAC	300
Qy	342	LysGluArgTrpGluAspValLysGluGluMetThrSerAlaLeuAlaThrMetArgVal	361
Db	301	AAGGAACGATGGGAGGATGTCAAGGAGGAGATGACCACTGCGCTTGGCCAGATGCGTGT	360
Qy	362	AspTyrGluGlnIleLysIleLysLysIleGluAspAlaSerAsnProLeuLeuLys	381
Db	361	GACTATGACGACATCAAGATAAAGAGATAGAGACGCATCCAAACCTCTGCTTCTCAAG	420
Qy	382	ArgArgLysLysAlaArgAlaLeuGluAlaAlaLeuAlaHis	396
Db	421	AGCGGAAGAAAGCTCGTGTGGAGGATGCGGCTCTCGCCCAAC	465
RESULT 5			
US-11-242-505A-40			
; Sequence 40, Application US/11242505A			
; Publication No. US2006009956A1			
; GENERAL INFORMATION:			
; APPLICANT: Carroll, Joseph M.			
; TITLE OF INVENTION: Methods and Compositions for Treating			
; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,			
; FILE REFERENCE: MPI2001-288P1RCP10MNIM			
; CURRENT APPLICATION NUMBER: US/11/242,505A			
; CURRENT FILING DATE: 2005-10-03			
; PRIOR APPLICATION NUMBER: US 10/290,078			
; PRIOR FILING DATE: 2002-11-07			
; PRIOR APPLICATION NUMBER: US 60/347,949			
; PRIOR FILING DATE: 2001-11-07			
; PRIOR APPLICATION NUMBER: US 10/320,351			
; PRIOR FILING DATE: 2002-12-16			
; PRIOR APPLICATION NUMBER: 60/341,606			
; PRIOR FILING DATE: 2001-12-17			
; NUMBER OF SEQ ID NOS: 48			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 40			
; LENGTH: 1740			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-11-242-505A-40			
Alignment Scores:			
Pred. No.:	8.8e-30	Length:	1740
Score:	522.00	Matches:	119
Percent Similarity:	56.3%	Conservative:	55
Best Local Similarity:	38.5%	Mismatches:	117
Query Match:	24.8%	Indels:	19
DB:	7	Gaps:	7





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Db      600  CCAGCCCGATGACACCACTCAAAATCGTGATTTTGGATCTCTATAAATGTGGAACAT 659
Qy      213  HieAsnSerLeuThrThrProCysTyrThrProTyrTyrValAlaProGluValLeuGly 232
Db      660  CAAGTGCTCATGAAGACAGTATGTGGAACCCAGGGTACTGCGCACCTGAAATCTTAGA 719
Qy      233  ProGluLysTyrAspLysSerCysAspMetTrpSerLeuGlyValIleMetTyrIleLeu 252
Db      720  GGTGTGCTATGACCTGAGGTGACATGTGGTCTGTAGGAATAATCACTACATCTTA 779
Qy      253  LeuCysGlyTyrProProPheTyrSerAsnHisGlyLeuAlaIleSerProGlyMetLys 272
Db      780  CTTTGTGGATTTGAACCATCTATGATGAAGAGC-----GATCATGTCATCTTC 830
Qy      273  ThrArgIleArgMetGlyGlnTyrGluPheProAsnProGluTrpSerGluValSerGlu 292
Db      831  AGGAGAAATTCGAATTGTGAATATTACTTTATCTCCCTGGTGGGATGAAGTATCTTA 890
Qy      293  GluValLysMetLeuIleArgAsnLeuLysThrGluProThrGlnArgMetThrIle 312
Db      891  AATGCCAAGGACTTGGTTCAGAAAATTAATTGTTTGGATCCAAAGAAACGGCTGACTACA 950
Qy      313  ThrGluPheMetAsnHisProTyrIle 321
Db      951  TTTCAAGCTCTCCAGCATCCGTGGGTC 977
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## RESULT 7

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US-10-449-902-20013
; Sequence 20013, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20013
; LENGTH: 1937
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK070346
; DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-20013
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## Alignment Scores:

Pred. No.:	9.56e-29	Length:	1937
Score:	508.50	Matches:	126
Percent Similarity:	49.6%	Conservative:	53
Best Local Similarity:	34.9%	Mismatches:	137
Query Match:	24.1%	Indels:	45
DB:	6	Gaps:	12

US-10-469-221-2 (1-386) x US-10-449-902-20013 (1-1937)

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Qy      1  SerGlnGlyGlnSerPro-----ProValPro 9
Db      45  TCCCAATCCCAATCCCAATCCCAACACCAAGCACCAACACCAACCAACCCCGG 104
Qy      10  PheProAlaProAlaProProGlnProProThrProAlaLeuProHisProProAla 29
Db      105  GCCCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCGCGG-----CAGCAGCCCGCATCT 158
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## RESULT 8

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US-10-449-902-21986
; Sequence 21986, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
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Qy      30  GlnProProProProPro-----ProGlnGlnPhePro-----GlnPheHisValLys 45
Db      159  CAGCCTCCCGCGCGCGCGCGGACACAGCGCCCGCAGCGCGCGCGCGCGGAG 218
Qy      46  SerGlyLeuGlnIleLysLysAsnAlaIleIleAspAspTyrLysValThr----- 62
Db      219  GATGGGGTGGGGGGGTGCTGGGGCGGCCCATGGAGGACGTCGTCGACCTACACCTTC 278
Qy      63  SerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLysArgThr 82
Db      279  GGGCGGAGGTGGGGGGGGGAGTTCCGGGTGACCTACCTCGCCACCAAGCCCAACC 338
Qy      83  GlnGluLysPheAlaLeuLysMetLeu-----GlnAspCys 94
Db      339  GGGCGAGCGTACCGCTCGAAGTCCATCGCGCGCGCAAGCTCGCGCGCGCGAGCCTC 398
Qy      95  ProLysAlaArgArgGluValGluLeuHisTrpArgAlaSerGlnCysProHisIleVal 114
Db      399  GACGAGCTCCGCGCGGAGGTCCACATCATGCACCTCACCGCCACCAACATCGTC 458
Qy      115  ArgIleValAspValTyrGluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMet 134
Db      459  GAGCTGCGCGCGCGCTACGAGGAC-----CGCCACTCCGTCACACCTCGTCATG 506
Qy      135  GluCysLeuAspGlyGlyGluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPhe 154
Db      507  GAGCTGCGAGGGCGCGCGAGCTTTGACCGCATCATGCCAGGGCCAC-----TAC 560
Qy      155  ThrGluArgGluAlaSerGluIleMetLysSerIleGlyAlaIleGlnTyrLeuHis 174
Db      561  TCCGAGCGCGCGCGCGCTCGCAGGAGATGTCCTCCGTCGTCACAGTCGCAC 620
Qy      175  SerIleAsnIleAlaHisArgAspValLysProGluAsnLeuLeuTyrThrSerLysArg 194
Db      621  TCCATGGGGTTCATGCACAGGACCTCAAGCCCGAGAACTTCCTTTCTCAACAAGCGC 680
Qy      195  ProAsnAlaIleLeuLysLeuThrAspPheGly-----PheAlaLysGluThrThr 211
Db      681  GAGGACTCCCGCTCAAGCCACCGATTTGGCTCTCCGTCCTTCTCAAGCCCGGTGAG 740
Qy      212  SerHisAsnSerLeuThrThrProCysTyrThrProTyrTyrValAlaProGluValLeu 231
Db      741  CAGTTCAGAGATCTTGTGGA-----AGTGCATATTATGTGCTCTCTGAGTCTTA 791
Qy      232  GlyProGluLysTyrAspLysSerCysAspMetTrpSerLeuGlyValIleMetTyrIle 251
Db      792  ---AAACGACTATATGAGCTGAGGCGAGACATATGAGTGTCTGGAGTTATCTTTATC 848
Qy      252  LeuLeuCysGlyTyrProProPheTyrSerAsnHisGlyLeuAlaIleSerProGlyMet 271
Db      849  CTTCTATCAGGGGTCTCTCATTTCTGGCGAGAAAC-----GAGGACGGTATA 896
Qy      272  LysThrArgIleArgMetGlyGlnTyrGluPheProAsnProGluTrpSerGluValSer 291
Db      897  TTTGATGCTGTTCTGCAAGGTCTATGCACTTCTCATCTGAAACCATCGCCTTCTATATCT 956
Qy      292  GluGluValLysMetLeuIleArgAsnLeuLysThrGluProThrGlnArgMetThr 311
Db      957  AGTGGTGCACAAAGACTTGGTCAAGCGGATGCTTCGGCAGGACCCCAAGAGGCGGTAACT 1016
Qy      312  IleThrGluPheMetAsnHisProTyrIleMetGlnSerThrLysValProGlnThrPro 331
Db      1017  GCTGCTGAATTTTGAACCAACCATCGATTAGAGAGGATGAGAGGCGGCCCAAGATAACCA 1076
Qy      332  Leu 332
Db      1077  CTT 1079
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; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21986
; LENGTH: 2641
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK072204
; DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-21986

Alignment Scores:
Pred. No.:          9,41e-28          Length:          2641
Score:              497.00             Matches:         132
Percent Similarity: 48.8%              Conservatives:    70
Best Local Similarity: 31.9%            Mismatches:      152
Query Match:        23.6%              Indels:          61
DB:                  6                  Gaps:            13

US-10-469-221-2 (1-396) x US-10-449-902-21986 (1-2641)

Qy   5 SerProValProPhe-----ProAlaProAlaProProGln----- 18
Db   821 AGCCCCCGAGCAGCGTCAAGATCGTCTCGACCGGACCGCGCTCGCGCGAGCAGGACG 880

Qy   19 ProProThrProAlaLeuProHisProAlaGlnProProProProProGlnGln 38
Db   881 CTTCAGTGCAGCGCGCGTCCGACTCCGGCGAGGCGCGCAGG-CGCGCGCGAGGGTG 939

Qy   39 PheProGlnPheHisValLysSerGly-----LeuGlnIleLys 51
Db   940 CGCGCGGTGAAGCGCGTCTCCAGCGCGCGGCTGCTCGCGTCTGCTGAAGCGCAAG 999

Qy   52 LysAsnAlaIleleAspAspTyrLysValThrSerGlnValLeuGlyLeuGlyIleAsn 71
Db   1000 ACGGAGAGTCTCAAGGACAAAGTACAGCCTG---GGCGCGAAGCTCGGCGAGGCGAGTTC 1056

Qy   72 GlyLysValLeuGlnIlePheAsnLysArgThrGlnGlyLysPheAlaLeuLysMetLeu 91
Db   1057 GGGACGAGTACCTGTCGTGGAGCGCGCCACCGGCAAGAGTTCGCTCGCAAGTCCATC 1116

Qy   92 -----GlnAspCysProLysAlaArgThrGlnGlyLysPheAlaLeuLysMetLeu 103
Db   1117 CTGAAGCGGAAGCTGGTCAACGACGACGCTCGAGGACGTCGCGCGGAGATCCAGATA 1176

Qy   104 HisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyrGluAsnLeu 123
Db   1177 ATGTACCACCTCGCGCGCCACCCCAACGTATCTCCATCAGGGCGCGCTACGAGGACGCC 1236

Qy   124 TyrAlaGlyArgLysCysLeuIleValMetGluCysLeuAspGlyGlyGluLeuPhe 143
Db   1237 GTGCC-----GTGCACCTCGTATGAGCTTCGCGCGCGCGCGAGCTGTTTC 1284

Qy   144 SerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSerGluIleMet 163
Db   1285 GACCGGATCTCCAGAAGGGGCAC-----TACACCGAGCGGAAGGCGCGGAGCTCGCC 1338

Qy   164 LysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHisArgAspVal 183
Db   1339 AGGGTCACTCGCGCGTCTCGAGGTGTGCACCTCCATCGGCGGTGATGCACCGGTGATCTC 1398

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Qy   184 LysProGluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeuLysLeuThrAsp 203
Db   1399 AGCCCGGAGAACCTCTCTTCGCGGACACGAGGAGCGCGCTCTCAAGACCATGAC 1458

Qy   204 PheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCysTyrThrPro 223
Db   1459 TTTGGTCTCTCCATTTTCTTTCGCCAGGTCAGATATTCATGATGTGTGTGGTAGCCCT 1518

Qy   224 TyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCysAspMetTrp 243
Db   1519 TACTATGTCGCGCAGAAAGTCTG---AAAAGAAATATGTCAGAGGAGAGATGTCG 1575

Qy   244 SerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProProPheTyrSerAsnHis 263
Db   1576 AGCGTGGTGTGATAATTACATCTTGTGTGTGGTGGCGCATTTTGGCAGAGAAC 1635

Qy   264 GlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyrGluPhePro 283
Db   1636 -----GAGCAGGGGTATATTGAAGAGGTTTTCATGCTAGTACTTGCATTTTCAG 1683

Qy   284 AsnProGluTrpSerGluValSerGluValLysMetLeuIleArgAsnLeuLys 303
Db   1684 TCAGAACCATGGCTCTGATCTCTGAAGGTGCCAAGATCTCGTAAGAGAAATGCTTGT 1743

Qy   304 ThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTyrIleMetGln 323
Db   1744 AGGACCCGAGAGAGATTCAGAGCTCATGAGTTTAAAGCATTCATCGGTCAGGTT 1803

Qy   324 SerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGluAspLysGlu 343
Db   1804 GGTGGTTTGGCTCTCGACAAAGCCCTG---GATTCGTCTTCTATCTCGTATGAAGCAA 1860

Qy   344 -----ArgTrpGluAspValLys 349
Db   1861 TTCTCAGTATGAATAAGTGAAAAAGATGGCTCTTAGGTCTATTCAGAGAACCTATCT 1920

Qy   350 GluGluMetThrSerAlaLeuAlaThrMet----- 359
Db   1921 GAAGCGAATTCGCGCGCTGAAGAAATGTTCAAGATGATCGACACAGACACAGATGGA 1980

Qy   360 ArgValAspTyrGluGlnIleLysIle-----LysLysIle 371
Db   1981 CAGTACCTTCGAAGAACTCAAGTTGGTGTCTGAAAAAAGTC 2022

RESULT 9
US-10-449-902-26866
; Sequence 26866, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26866
; LENGTH: 2524
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK102308
; DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-26866

Alignment Scores:

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Pred. No.: 1.3e-26 Length: 2524
Score: 481.00 Matches: 116
Percent Similarity: 50.9% Conservative: 57
Best Local Similarity: 34.1% Mismatches: 123
Query Match: 22.8% Indels: 44
DB: 6 Gaps: 8

US-10-469-221-2 (1-396) x US-10-449-902-26866 (1-2524)

QY 24 LeuProHisProAlaGlnProProPro----- 33
Db 647 CTGGGTGCGCGCAATGACGCGGAGCCGCGGAGCGGCGGCGGACGACGCAAT 706
QY 34 -----ProProGlnGlnPheProGlnPheHisValLysSerGly 47
Db 707 GCGAAGCGGAAGCTGGCGCGCGCGGTGACGCGCGGAGGTGCGCGGTGCGGTG 766
QY 48 LeuGlnIleLysAsnAlaIleAspTyrLysValThrSerGlnValLeuGly 67
Db 767 CTCCCGCACAGACGCGGACGTCGCGGACCATACCGCATC---GGGAAGAGCTCGG 823
QY 68 LeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLysArgThrGlnGluLysPheAla 87
Db 824 CAGGGCGAGTTCGGGACGAGTACCTGCTGCTGACAAAGCGGCGCGGAGTTCGCG 883
QY 88 LeuLysMetLeu-----GlnAspCysProLysAlaArgArg 99
Db 884 TGCAAGTCCATCCCAAGCGGAAGCTGCTGTGCGGAGGACTACGAGGAGCTGTGCGC 943
QY 100 GluValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspVal 119
Db 944 GAGATCCAGATCATGACCACTCTCTCGAGCACCAACGTCGTCGCGATCCCGCGGCGC 1003
QY 120 TyrGluAsnLeuTyrAlaGlyArgLysCysLeuIleValMetGluCysLeuAspGly 139
Db 1004 TACGAGGACGCGTG-----TTGCTCCACATGTCATGAGCTCTGCGCGCGC 1051
QY 140 GlyGluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAla 159
Db 1052 GCGGAGCTCTTCGACGCGATCTGCGCAAGGGCCAC-----TACACCGAGCGCGCGC 1105
QY 160 SerGluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAla 179
Db 1106 GCGAGCTATCCGCACCATCTGCGCGTCTGCGGATGCCACTGCTCGCGGTCATG 1165
QY 180 HisArgAspValLysProGluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeu 199
Db 1166 CACGCGGACCTCAAGCCGAGAACTTCTCTCGCCAGCGCCGCGGAGGACGCCCCCTC 1225
QY 200 LysLeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrPro 219
Db 1226 AAGGCCACTGATTTGCGGCTCTCTGTTTCTACAAGCCTGCTGATAAGTTCTCTGAT 1285
QY 220 CysTyrThrProTyrTrpValAlaProGluValLeu-----GlyProGluLys 235
Db 1286 GTTGGGAGCCCTATTATGTTGACCTGAGTACTTCAGAAATGCTATGTTCCAGATCT 1345
QY 236 TyrAspLysSerCysAspMetTrpSerLeuGlyValIleMetTyrIleLeuLysCysGly 255
Db 1346 -----GATGCTCGAGTGTGGGTAACTTCTTACATTTTGTATGTGTT 1390
QY 256 TyrProProPheTyrSerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIle 275
Db 1391 GTTCCACCAATTTGGGCGAA-----ACTGAAGCTGGAATTTTCAGCGAGATT 1438
QY 276 ArgMetGlyGlnTyrGluPheProAsnProGluTrpSerGluValSerGluGluValLys 295
Db 1439 CTAGGAGCAAACTTGATTTGATCTGAACCTTGGCTAGCATCTCTGACAGTGTATA 1498
QY 296 MetLeuIleArgAsnLeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPhe 315
Db 1499 GATCTAGTCGTAATATGCTTTGCGGGATCTTACAAGAGACTTACAGCCCATGAGGTT 1558
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QY 316 MetAsnHisProTrpIleMetGlnSerThrLysValProGlnThrProLeuHisThrSer 335
Db 1559 CTCTGTCTCATTCATGGATTGTTGATGATGCTGTGGCACCTGACAAAGCTATTGATTCT 1618

RESULT 10
US-10-505-928-350
; Sequence 350, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 350
; LENGTH: 3982
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928-350

Alignment Scores:
Pred. No.: 3.1e-26 Length: 3982
Score: 479.00 Matches: 119
Percent Similarity: 50.7% Conservative: 68
Best Local Similarity: 32.2% Mismatches: 125
Query Match: 22.7% Indels: 57
DB: 6 Gaps: 13

US-10-469-221-2 (1-396) x US-10-505-928-350 (1-3982)

QY 10 PheProAlaProAlaProProGlnProProThrPro----- 22
Db 1281 TTCACAGCGGAGCGCCACAGACTCTCTCTGGGTCCCCCGAGTGCAACGCTCATCAC 1340
QY 23 -----AlaLeuProHisProAlaGln----- 30
Db 1341 CTGTTTAGAGATTACAGTTTGTGGCTCAAGCCTGATCCAGGAGCCTCACAGCAAGAT 1400
QY 31 -----ProProProProProGlnGlnPhe-----ProGlnPheHisVal 44
Db 1401 CTGCACAAAGTCCAGCTTACCACATCGTCGACAGCTTACCGGGAACACATCCACTTC 1460
QY 45 LysSerGlyLeuGlnIleLysLysAsnAlaIleAspTyrLysValThrSerGln 64
Db 1461 ACCGATGGCTACGAGATCAAGGAGGACATCGGGGTGGGTCTCTACTCACTGTGCAAGCA 1520
QY 65 valLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLysArgThrGlnGlu 84
Db 1521 TGTGTG-----CATAAAGCCACAGACACC 1544
QY 85 LysPheAlaLeuLysMetLeuGlnAspCysProLysAlaArgArg-----Glu 100
Db 1545 GAGTATGCGCTGAAGATCATTTGAT-----AAGAGCAAGAGAGACCCCTCGGAAGAG 1595
QY 101 valGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr 120
Db 1596 ATTGAGATCTCTCTGCGGTACGCGCCAGCACCCCAACATCATCACCTTCAAGGATGTCTAT 1655
QY 121 GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly 140
Db 1656 GATGAT-----GGCAAGTTTGTGTACTGTAATGAGAGTGTATCGGTGGTGGG 1703
QY 141 GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer 160
Db 1704 GAGCTCTGAGCCGCTCTCCCGCAG-----AGATACTTCTCGGAGCGCAAGCCAGT 1757
QY 161 GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis 180
Db 1758 GAGGTCTGTGCAACCATCACCAAGCATGAGTACTTCCAGGGGGTGTGTTTTCAT 1817
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Db 303 GCCCAGTTTGGTGTACGCTACCTCGTAACCTCACAAGAGACGAAACACAGGTCGCTTGC 362
Qy 89 LysMetLeu-----GlnAspCysProLysAlaArgGlu 100
Db 363 AAGTCAATCCCTACCGCGCGCTTGTTCACAAAGACGACATTGAAGATGTTCCGCCGTGAA 422
Qy 101 ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr 120
Db 423 GTCCAGATTATGCACCATCTCAGCGGTCCACCGAACATAGTGGACTTGAAGGAGCCTAC 482
Qy 121 GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly 140
Db 483 GAGGAC-----AGACACTCTCTGAATCTGATAATGAGATTGTGTAAGGAGGG 530
Qy 141 GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer 160
Db 531 GAATTTGTCGATAGATCATTTCTAAAGGT-----CTTTACTCAGAGAGAGCTGCTGCG 584
Qy 161 GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis 180
Db 585 GATTTGTGTAGGCAGATGGTGTGTGTCATAGTGTCTATGGGTGTAATGCAC 644
Qy 181 ArgAspValLysProGluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeuLys 200
Db 645 CGAGACTTGAAGCCGAAACTTTCTCTTCTTAGTAAAGATGAGAACTCACCATTTGAAA 704
Qy 201 LeuThrAspPheGly-----PheAlaLysGluThrThrSerHisAsnSerLeuThr 217
Db 705 GCTACAGACTTTGGTCTCTCTGTCTCTTCAAGCCAGGTGATAGTTTAAGGATCTTTGTT 764
Qy 218 ThrProCysTyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAsp 237
Db 765 GGA-----AGTGCATACTATGTGCCCCAGAGTTCTA---AAACGGAACTATGGA 812
Qy 238 LysSerCysAspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrPro 257
Db 813 CCAGAGGCTGATATCTGGAGTGTGCTGTGATCTTATACATCCTTCTCAGTGGTGTTCGG 872
Qy 258 ProPheTyrSerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMet 277
Db 873 CCTTTCTGGGGAGAAAAT-----GAAACGGGGGATCTTTGTATGCCCATTTCTCAA 920
Qy 278 GlyGlnTyrGluPheProAsnProGluTrpSerGluValSerGluGluValLysMetLeu 297
Db 921 GGGCACTTGATTTTCAGCTGATCCATGCCAGCACATATCAGATGGTGGCCAAAGATCTT 980
Qy 298 IleArgAsnLeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsn 317
Db 981 GTGAGGAAATGTTAAATATATACCCCTAAAGATCGCTTACAGCTGCGGAAGTGTCTAAAT 1040
Qy 318 HisProTrpIleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgVal 337
Db 1041 CATCCGCGGATTAGAGAGATGGGAGGCGATCAGACAAACCGCTTGACAATGCG---GTG 1097
Qy 338 LeuLysGluAspLysGlu-----ArgTrpGluAspValLysGluMetThrSerAla 355
Db 1098 TTATCCAGATGAACAACATTCGGCGCATGAACAACATAAATAAATAATGGCCCTGAAGTT 1157
Qy 356 LeuAlaThrMetArgValAspTyrGluGlnIleLysIleLysLysIle 371
Db 1158 ATCGCTGAGAACCTTTCTGAAGAAGAAATCATTTGTTCTTAAAGAGATG 1205
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Job time : 62 secs

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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Title: US-10-469-221-2

Perfect score: 2106

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Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	1991.5	94.6	2258	3	US-09-016-434-1415
3	1391	66.0	2481	3	US-09-016-434-1088
4	1391	66.0	2482	3	US-09-949-016-5682
5	1391	66.0	2509	3	US-09-949-016-660
6	1333	63.3	1333	3	US-09-142-551A-1
7	540	25.6	3061	4	US-09-880-107-2146
8	536	25.5	1671	3	US-09-733-388-5

9	536	25.5	1671	3	US-10-446-175-5	Sequence 5, Appli
10	532.5	25.3	1733	3	US-09-620-312D-526	Sequence 536, App
11	529.5	25.1	1694	3	US-09-579-664B-3	Sequence 3, Appli
12	529.5	25.1	1694	3	US-10-355-975A-3	Sequence 3, Appli
13	529.5	25.1	1694	5	US-09-980-464-3	Sequence 3, Appli
14	523	24.8	1442	3	US-09-949-016-1590	Sequence 1590, Ap
15	523	24.8	1442	3	US-09-949-016-1591	Sequence 1591, Ap
16	523	24.8	1480	3	US-09-016-434-1454	Sequence 1454, Ap
17	498	23.6	2447	3	US-09-960-643-1	Sequence 1, Appli
18	496.5	23.6	1074	3	US-09-733-388-3	Sequence 3, Appli
19	496.5	23.6	1074	3	US-10-446-175-3	Sequence 3, Appli
20	496.5	23.6	1158	3	US-09-733-388-1	Sequence 1, Appli
21	496.5	23.6	1158	3	US-10-446-175-1	Sequence 1, Appli
22	486	23.1	1584	3	US-09-799-451-205	Sequence 205, App
23	484.5	23.0	2165	3	US-09-620-312D-809	Sequence 2, Appli
24	484.5	23.0	3471	2	US-08-715-568A-2	Sequence 5, Appli
25	474.5	22.5	1458	3	US-09-230-896C-5	Sequence 1939, Ap
26	467	22.2	3119	3	US-09-949-016-1939	Sequence 1, Appli
27	464.5	22.1	2061	3	US-09-800-960-1	Sequence 1, Appli
28	464.5	22.1	2061	3	US-10-096-960-1	Sequence 12, Appl
29	454.5	21.6	1282	2	US-08-878-989-12	Sequence 12, Appl
30	454.5	21.6	1282	3	US-09-272-796-12	Sequence 933, App
31	454.5	21.6	1282	3	US-09-016-434-953	Sequence 1, Appli
32	443	21.0	1545	3	US-09-841-683-1	Sequence 1, Appli
33	443	21.0	1545	3	US-10-620-845-1	Sequence 3, Appli
34	443	21.0	2001	3	US-09-841-683-3	Sequence 3, Appli
35	443	21.0	2001	3	US-10-620-845-3	Sequence 1, Appli
36	443	21.0	2218	3	US-09-820-790B-1	Sequence 1, Appli
37	443	21.0	2287	3	US-10-104-047-1539	Sequence 1339, Ap
38	441	20.9	1735	3	US-09-746-694-3	Sequence 3, Appli
39	441	20.9	1858	3	US-09-529-093A-1	Sequence 1, Appli
40	441	20.9	1858	3	US-09-529-154-1	Sequence 1, Appli
41	441	20.9	1858	3	US-10-185-182A-1	Sequence 1, Appli
42	440.5	20.9	1991	3	US-10-104-047-1214	Sequence 1214, Ap
43	438	20.8	2230	3	US-09-828-313-26	Sequence 26, Appl
44	435.5	20.7	2298	3	US-09-975-326-3	Sequence 3, Appli
45	435.5	20.7	2298	3	US-10-217-357-3	Sequence 3, Appli

#### ALIGNMENTS

#### RESULT 1

US-09-023-655-1397  
; Sequence 1397, Application US/09023655  
; Patent No. 6607879  
; GENERAL INFORMATION:  
; APPLICANT: Cocks, Benjamin G.  
; APPLICANT: Susan G. Stuart  
; APPLICANT: Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
; TITLE OF INVENTION: EXPRESSION  
; NUMBER OF SEQUENCES: 1508  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM: disk  
; MEDIUM TYPE: Floppy  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/023,655  
; FILING DATE: HEREWITH  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:

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; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1397:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1336 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: 9407074
; US-09-023-655-1397

Alignment Scores:
Pred. No.: 9.88e-186 Length: 1336
Score: 2078.00 Matches: 393
Percent Similarity: 99.2% Conservative: 0
Best Local Similarity: 99.2% Mismatches: 3
Query Match: 98.7% Indels: 0
DB: 3 Gaps: 0

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Db 1 TCCAGGGCCAGAGCCCGCGGTGCGGTTCGCCGCCCGCGCGCGCGCGCGCGCC 60
Qy 21 ThrProAlaLeuProHisProProAlaGlnProProProProProGlnGlnPhePro 40
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Qy 41 GlnPheHisValLysSerGlyLeuGlnLysLysValLysLysAlaLysLysLys 60
Db 121 CAGTTCACGTCAAGTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
Qy 61 ValThrSerGlnValLeuGlyLeuGlyLysLysValLysLysValLysLysLys 80
Db 181 GTACACGACCGAGTCTCTGGGCGTGGCGCATCAACGGCAAGTTTTCAGAGATCTTCAACAAG 240
Qy 81 ArgThrGlnGlnLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaArgArgGlu 100
Db 241 AGGACCCAGGAGAAATTCGCCCTCAAAATGCTTCAGGACTGCCCAAGGCCCGCAGGGAG 300
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Db 301 GTGGAGCTGACCTGGCGGGGCTCCAGTGGCGCGCGCGCGCGCGCGCGCGCGCG 360
Qy 121 GluAsnLeuTyrAlaGlyArgLysCysLeuLeuLeuValMetGluCysLeuAspGlyGly 140
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Db 481 GAAATCATGAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCATCAATGCGCCAT 540
Qy 181 ArgAspValLysProGluAsnLeuLeuTyrThrSerLysArgProAsnAlaLysLys 200
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Db 601 CTCACCTGACTTGGCTTTGGCAGAGAAACACCGAGCCACCACTCTTTGACCACTCTCTGT 660
Qy 221 TyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys 240
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Db 661 TATACACCGTACTATGTGCTCCAGAAAGTGTGGTCCAGAGAGTATGACAAAGTCTGT 720
Qy 241 AspMetTyrSerLeuGlyValLysMetTyrLysLeuLeuCysGlyTyrProProPheTyr 260
Db 721 GACATGTGTGCTCTGGTGTGCATGATGATTCATCTGCTGTGGTATCCCCCTTCTAC 780
Qy 261 SerAsnHisGlyLeuAlaLysSerProGlyMetLysThrArgLysMetGlyGlnTyr 280
Db 781 TCCAACGCGGCTTGCATCTCTCCGGCATGAGAGATCGCATCCGAATGGGCCAGTAT 840
Qy 281 GluPheProAsnProGluTyrSerGluValSerGluLysValLysMetLeuLysArgAsn 300
Db 841 GAATTTCCCAACCCAGAAATGTCAGAAATGTCAGAGAGAGTGAAGATGCTCATTCGGAAT 900
Qy 301 LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTyr 320
Db 901 CTGCTGAAACACAGAGCCACCCAGAGAAATGACCATCACCGAGTTTATGAACACCCCTTG 960
Qy 321 IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGlu 340
Db 961 ATCATGCAATCAACAAAGGTCCCTCAAAACCCCACTGCACACCGCGGGTCTTGAAGAG 1020
Qy 341 AspLysGluArgTyrGluAspValLysGluMetThrSerAlaLeuAlaThrMetArg 360
Db 1021 GACAAGGCGGTGGGAGGATGTCAGAGGAGGAGATGACCAAGTGGCTTGGCCCAATGCGC 1080
Qy 361 ValAspTyrGluGlnLysLysLysLysLysLysLysLysLysLysLysLysLysLys 380
Db 1081 GTTGACTACGAGCAGATCAAGATAAAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1140
Qy 381 LysArgGlyLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 396
Db 1141 AAGAGCGGAAGAAAGTCTGGGCGCTGGAGGCTGGCGCTCTGGCCAC 1188

RESULT 2
US-09-016-434-1415
; Sequence 1415, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1415:
; SEQUENCE CHARACTERISTICS:
```

; LENGTH: 2258 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; IMMEDIATE SOURCE:  
 ; LIBRARY: GENBANK  
 ; CLONE: 9530089  
 ; US-09-016-434-1415

## Alignment Scores:

Pred. No.: 2,85e-177 Length: 2258  
 Score: 1991.50 Matches: 396  
 Percent Similarity: 69.0% Conservative: 0  
 Best Local Similarity: 69.0% Mismatches: 0  
 Query Match: 94.6% Indels: 178  
 DB: 3 Gaps: 1

US-10-469-221-2 (1-396) x US-09-016-434-1415 (1-2258)

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Qy 1 SerGlnGlyGlnSerProValProPheProAlaProAlaProProGlnProPro 20
Db 391 TCCAGGGCCAGAGCCCGCGGTCCGTTCCCGCCCGCGCCCGCGAGCCCCC 450

Qy 21 ThrProAlaLeuProHisProAlaGlnProProProProGlnGlnPhePro 40
Db 451 ACCCGTCCCTGCCGACCCCGCGCGCAGCGCGCGCGCGCGCGCGAGCTCCG 510

Qy 41 GlnPheHisVallysSerGlyLeuGlnIleIleIleIleIleIleIleAsp 60
Db 511 CAGTTCACGTCAGTCCGCGCTCCAGATCAAGAGAACGCCATCATCGATGAC 570

Qy 61 ValThrSerGlnValLeuGlyLeuGlyLeuGlyLeuGlyLeuGlyLeuGly 80
Db 571 GTACACAGCCAGGTCTTGGGGCTGGGCATCAACGGCAAGTTTGCAGATCTT 630

Qy 81 ArgThrGlnGlyPheAlaLeuLysMetLeuGlnAspCysProLysAlaArgGlu 100
Db 631 AGGACCCAGGAGAAATTCGCCCTCAAAATGCTTCAGGACTGCCCAAGGCGC 690

Qy 101 ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleVal 120
Db 691 GTGAGCTGACCTGGCGGGCTCCAGTGGCGGCACATCGTACGGATCGTGATC 750

Qy 121 GluAsnLeuTrpAlaGlyArgLysCysLeuLeuIleValMetGluCysLeu 140
Db 751 GAGATCTGTACGAGGAGGAGTGTCTGCTGATGTCATGGAATGTTGGACGTT 810

Qy 141 GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArg 160
Db 811 GAACCTTTAGCCGAAATCCAGGATCGAGGAGACCAGGCATTCACAGAAAGA 870

Qy 161 GluIleMetLysSerIleGlyGluAlaIleGlnTrpLeuHisSerIleAsn 180
Db 871 GAAATCATGAAGACATCGGTAGGCCATCCAGTATCTGATTCATCAATCAAT 930

Qy 181 ArgAspVallysProGluAsnLeuLeuTrpThrSerLysArgProAsnAla 200
Db 931 CGGGATGTCAGGCTGAGATCTCTTATACCTCCAAAGGCCCAACGCCATCT 990

Qy 201 LeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThr 220
Db 991 CTCACGTACTTGGCTTGGCAGGAAACCAACAGCCACCAACTCTTTGACCA 1050

Qy 221 TyrThrProTyrValAlaProGluValLeuGlyProGluLysTyrAspLys 240
Db 1051 TATACACCGTACATGTGGCTCCAGAAAGTGTGGTCCAGAGAGTATGACAA 1110

Qy 241 AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrPro 260
Db 1111 GACATGGTTCCTGGGTGTTCATCATGTATCTGTGTGGTATCCCCCTTCT 1170

Qy 261 SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMet 280

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Db 1171 TCCAAACCAACGCGCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 1230
Qy 281 GluPheProAsnProGluTrpSerGluValSerGluValSerGluValSerGluValSer 300
Db 1231 GAATTTCCCAACCCAGAAATGGTCAGAGATATCAGAGGAAGTGAAGATGCTCATTTCCGAAT 1290
Qy 301 LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTrp 320
Db 1291 CTGCTGAAGAACAGAGCCACCCAGAGAAATGACCATCACCGAGTTTATGAACCAACCCCTTGG 1350
Qy 321 IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGlu 340
Db 1351 ATCATGCAATCAACAAAGGTCCCTCAAAACCCCATGTCACACCCAGCCGCGTCTGAAGAG 1410
Qy 341 AspLysGluArgTrpGluAspValLys----- 349
Db 1411 GACAGGAGCGGTGGGAGGATGCAAGGGGTGTTCTTCATGACAAAGAACAGGACCAAGGCC 1470
Qy 349 ----- 349
Db 1471 ACTTGGCTGACAGGTTGTGAGCAGAGGATTTCTGTGTTCTGTCCTCAAACTCAGTGTCT 1530
Qy 349 ----- 349
Db 1531 TCTTAGAATCCTTTTATTTCCCTGGGTCTCTAATGGGACCTTAAAGACCATCTGTTATCAT 1590
Qy 349 ----- 349
Db 1591 CTTCTCATTTTGGAGAAGAGAAACTGAGGCCAGAGCGGAGGCGAGCTGTGCTCAAGGTC 1650
Qy 349 ----- 349
Db 1651 ACGAGCTGTGTGACTGTTGGGGCAGACCGGACCCAGGTTTCTGACTCTCTGGCCCCAAGT 1710
Qy 349 ----- 349
Db 1711 CTCTTCTCCTATCTCTGCGGATCACTGGGGGCTCTCAGGGAAACAGCAGCAGTGCCATA 1770
Qy 349 ----- 349
Db 1771 GCCAGGCTCTCTGCTGCCAGCGCTGGGGTGAGGCTGCCGTTGTACGCGTGGACCACTAA 1830
Qy 349 ----- 349
Db 1831 CCAGCCCGTCTTCTCTCTCTGCTCCACCCCTCCCGCTCACCTGCCCTTGTGTCTCTG 1890
Qy 349 ----- 349
Db 1891 TCTCTCACTGTCTCTTCTGCTGTCTCTACTGTCTTCTTGGCTCTCTCTGTACCCCTTCCT 1950
Qy 350 -----GluGluMetThrSerAlaLeuAlaThrMetArgValAspTy 363
Db 1951 GGTGTGCGCGTGGCCCCAGGAGGATGACAGTGTCTTGGCCCAATGCGGTGACTA 2010
Qy 363 rGluGlnIleLysIleLysLysIleGluAspAlaSerAsnProLeuLeuLysArgAr 383
Db 2011 CGAGCAGATCAAGATAAAAAAGATTGAAGATGATCAACCCCTCTGCTGCTGAAGAGCG 2070
Qy 383 gLysLysAlaArgAlaLeuGluAlaAlaLeuAlaHis 396
Db 2071 GAAGAAAGCTCGGGCCCTGGAGGCTGCGGCTCTGGCCCCAC 2110

```

## RESULT 3

US-09-016-434-1088  
 ; Sequence 1088, Application US/09016434  
 ; Patent No. 6500938  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Janice Au-Young  
 ; APPLICANT: Jeffrey J. Seilhamer  
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
 ; TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
 ; NUMBER OF SEQUENCES: 1490  
 ; CORRESPONDENCE ADDRESS:



; SEQ ID NO 5682  
; LENGTH: 2482  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-5682

## Alignment Scores:

Pred. No.: 9,15e-121 Length: 2482  
Score: 1391.00 Matches: 265  
Percent Similarity: 80.2% Conservative: 50  
Best Local Similarity: 67.4% Mismatches: 56  
Query Match: 66.0% Indels: 22  
DB: 3 Gaps: 3

US-10-469-221-2 (1-396) x US-09-949-016-5682 (1-2482)

```
Qy 1 SerGlnGlyGlnSerProValProPheProAlaProPheProGlnProPro 20
Db 107 GCAGAGGAGCAGGGGGCCCTGTGCC-----CCGCCAGTTGCACCCGCG 151
Qy 21 ThrProAlaLeuProHisProAlaGlnProProProProGlnGlnPhePro 40
Db 152 GGACCCGCTGGGGCGTCTCCGGGGGGGGGGGAGGCC----- 193
Qy 41 GlnPheHisValLysSerGlyLeuGlnLeuLysLysAsnAlaIleAspTyrLys 60
Db 194 -----AAGAAGTACGCAGTGACCGACGACTACCGAG 223
Qy 61 ValThrSerGlnValLeuGlyLeuGlyLeuGlyLeuGlyValLeuGlnIlePheAsnLys 80
Db 224 TTGTCCAAGCAGGTGCTGGGCTGTGAACGCGAAAGTGCTGGAGTGCTTCCATCGG 283
Qy 81 ArgThrGlnGluLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaArgGlu 100
Db 284 CGCATGACAGAGAGTGTGCCCTGAAGCTCTGTATGACAGCCCAAGCCCGCAGGAG 343
Qy 101 ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr 120
Db 344 GTAGACCATCACTGGCAGGCTTCTGGCGGCCCCCATATTGCTGCATCTCGATGTGTAT 403
Qy 121 GluAsnLeuTyrAlaGlyArgLysCysLeuLeuLeuValMetGluCysLeuAspGlyGly 140
Db 404 GAGAACATGACACCATGGCAAGCGTGTCTCTCATCATCATGGAATGCATGGAAGTGGT 463
Qy 141 GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer 160
Db 464 GAGTGTTCACAGAGATTCAGAGCGTGGCGACAGCGCTTCACTGAGAGAAAGCTGCA 523
Qy 161 GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis 180
Db 524 GAGATAATGCGGGATATTGGCACTGCCATCCAGTTTCTGCACAGCCCAATTAACATTGCCAC 583
Qy 181 ArgAspValLysProGluAsnLeuTyrThrSerLysArgProAsnAlaIleLeuLys 200
Db 584 CGAGATGTCAAGCCCTGAAACCTACTACACATCTAAGGAGAAAGACGCGAGTCTTAAG 643
Qy 201 LeuThrAspPheGlyPheAlaLysGlnThrThrSerHisAsnSerLeuThrThrProCys 220
Db 644 CTCACCGATTGGCTTGTCTAGAGACACAC-----CMAAATGCCCTGCACAGACCTGCG 700
Qy 221 TyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys 240
Db 701 TATACTCCCTATTATGTGGCCCTGAGGCTCGGTCCAGAGAGATGACAAAGTCAATGT 760
Qy 241 AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProProPheTyr 260
Db 761 GACATGTGCTCCCTGGGTGTCATCATGTACATCTCTTGTGCTTCCACCCCTTCTAC 820
Qy 261 SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr 280
Db 821 TCCAAACGCGCCAGGCCATCTCCCGGGGATGAAGAGGAGATTCGCTGGCGCAGTAC 880
Qy 281 GluPheProAsnProGluTrpSerGluValSerGluGluValLysMetLeuIleArgAsn 300
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Db 881 GGCTTCCCAATCTCTGAGTGGTCAGAAAGTCTCTGAGGATGCCAAGACGCTGATCGGCTC 940
Qy 301 LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTyr 320
Db 941 CTGTTGAAGACAGACCCCAAGAGGCTGACCATCACTCAGTTTCATGAACCAACCCCTGG 1000
Qy 321 IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGlu 340
Db 1001 ATCAACCAATCGATGTAGTGCACAGACCCCACTCCACAGCGCCGAGTGTGCAGAG 1060
Qy 341 AspLysGluArgTrpGluAspValLysGluGluMetThrSerAlaLeuAlaThrMetArg 360
Db 1061 GACAAAGACCACTGGGACGAAGTCAAGGAGGAGATGACCATGCTGCTTGGCCACTATGCG 1120
Qy 361 ValAspTyrGluGlnIleLysIleLysIleGluAspAlaSerAsnProLeuLeuLeu 380
Db 1121 GTAGACTACCAAGTGAAGATCAAGGACCTTAAGACCTTAAACAACCGCTCTCTCAAC 1180
Qy 381 LysArgArgLysLysAlaArgAlaLeuGluAlaAla 393
Db 1181 AAGAGGAGAAAGACGAGGAGGAGGCTCTCTGCTCA 1219
```

## RESULT 5

US-09-949-016-660  
; Sequence 660, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14

; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: Fast-Seq for Windows Version 4.0  
; SEQ ID NO 660

; LENGTH: 2509  
; TYPE: DNA

; ORGANISM: Human  
US-09-949-016-660

## Alignment Scores:

Pred. No.: 9.3e-121 Length: 2509  
Score: 1391.00 Matches: 265  
Percent Similarity: 80.2% Conservative: 50  
Best Local Similarity: 67.4% Mismatches: 56  
Query Match: 66.0% Indels: 22  
DB: 3 Gaps: 3

US-10-469-221-2 (1-396) x US-09-949-016-660 (1-2509)

```
Qy 1 SerGlnGlyGlnSerProValProPheProAlaProPheProGlnProPro 20
Db 134 GCAGAGGAGCAGGGGGCCCTGTGCC-----CCGCCAGTTGCACCCGCG 178
Qy 21 ThrProAlaLeuProHisProAlaGlnProProProProGlnGlnPhePro 40
Db 179 GGACCCGCTGGGGCGTCTCCGGGGGGGGGGGAGGCC----- 220
Qy 41 GlnPheHisValLysSerGlyLeuGlnIleLysLysAsnAlaIleAspTyrLys 60
Db 221 -----AAGAAGTACGCAGTGACCGACGACTACCGAG 250
Qy 61 ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLys 80
Db 251 TTGTCCAAGCAGGTGCTGGGCTGTGAACGCGAAAGTGTGGAGTGTCTTCCATCGG 310
```

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Qy 81 ArgThrGlnGluLysPheAlaLeuLysMetIeuGlnAspCysProLysAlaAArgGlu 100
Db 311 CGCACTGGACAGAGTGTGGCTTCTGATGACAGCCCAAGAGCGCGGCGAGAG 370
Qy 101 ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr 120
Db 371 GTAGACCATCACTGGCAGGCTTCTGGCGGCCCATATTGCTGCACTCTGGATGTGTAT 430
Qy 121 GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly 140
Db 431 GAGAACATGCACCATGCCAAGCGTGTCTCTCATCATCATGGAATGCATGGAAGGTGGT 490
Qy 141 GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer 160
Db 491 GAGTTGTTACAGGATTACAGGAGCGTGGCAGCAGGCTTCTACGTGAGAGAAAGCTGCA 550
Qy 161 GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis 180
Db 551 GAGATAATGGGNTATTGGCACTGCCATCAGTTTCTGCACAGCCATAACATTGCCAC 610
Qy 181 ArgAspValLysProGluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeuLys 200
Db 611 CGAGATGTCAAGCTCAAGACCTACTCTACACATCTAAGGAGAAAGACGAGTCTTAAG 670
Qy 201 LeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCys 220
Db 671 CTCACCGATTTTGGCTTTGTCAAGGAGACCAACC---CAAAATGCCCTCGACAGACCCCTGC 727
Qy 221 TyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys 240
Db 728 TATACTCCCTATTATGTGGCCCTGAGGTCTGGGTCCAGAGAAATATGACAGTCAATGT 787
Qy 241 AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProProPheTyr 260
Db 788 GACATGTGGTCCCTGGGTGTATCATGTACATCTCTTGTGGCTTCCCAACCTTCTAC 847
Qy 261 SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr 280
Db 848 TCCAACACGGGCCAGGCCATCTCCCGGGATGAAGAGGAGGATTCGCCTGGGCGCAGTAC 907
Qy 281 GluPheProAsnProGluTrpSerGluValSerGluGluValLysMetLeuIleArgAsn 300
Db 908 GGCTTCCCAATCCTGAGTGGTCAGAAGTCTCTGAGGATGCCAAGCAGCTGATCCGCTC 967
Qy 301 LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTrp 320
Db 968 CTGTTGAAGACAGACCCCAAGAGGCTGACCATCACTCAGTTCAATGAACCAACCCCTGG 1027
Qy 321 IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGlu 340
Db 1028 ATCAACCAATCGATGGTAGTGCCACAGACCCCACTCCACACGGCGCGAGTGGTGCAGAG 1087
Qy 341 AspLysGluArgTrpGluAspValLysGluGluMetThrSerAlaLeuAlaThrMetArg 360
Db 1088 GACAAACACCACTGGGACGAGTCAAGAGAGATGACCAAGTGCCTTGGCCCATATGCGG 1147
Qy 361 ValAspTyrGluGlnIleLysIleLysLysIleGluAspAlaSerAsnProLeuLeuLeu 380
Db 1148 GTAGACTACGACCAAGGTGAAGATCAAGGACCTGAAGACCTTAACAACCGGCTCTCAAC 1207
Qy 381 LysArgArgLysLysAlaArgAlaLeuGluAlaAla 393
Db 1208 AAGAGGAGAAAAAGCAGGCGAGCGAGCTCTCTGCTCCTCA 1246
```

## RESULT 6

US-09-142-551A-1

; Sequence 1, Application US/09142551A

; Patent No. 6218136

; GENERAL INFORMATION:

; APPLICANT: KUNAR, SANJAY

; APPLICANT: LIVI, GEORGE P.

; APPLICANT: MCLAUGHLIN, MEGAN M.

```
; APPLICANT: YOUNG, PETER R.
; TITLE OF INVENTION: METHODS OF THE IDENTIFICATION OF
; FILE OF INVENTION: PHARMACEUTICALLY ACTIVE COMPOUNDS
; FILE REFERENCE: P50448
; CURRENT APPLICATION NUMBER: US/09/142,551A
; CURRENT FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: PCT/US97/04256
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,286
; PRIOR FILING DATE: 1996-03-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1333
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-142-551A-1
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## Alignment Scores:

Pred. No.:	1,05e-115	Length:	1333
Score:	1333.00	Matches:	263
Percent Similarity:	79.0%	Conservative:	50
Best Local Similarity:	66.4%	Mismatches:	56
Query Match:	63.3%	Indels:	28
DB:	3	Gaps:	5

US-10-469-221-2 (1-396) x US-09-142-551A-1 (1-1333)

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Qy 1 SerGlnGlyGlnSerProValProPheProAlaProAlaProProGlnProPro 20
Db 53 GCAGAGGACGAGGGGGCCCTGTGCC-----CGCCAGTTGCACCGCGC 97
Qy 21 ThrProAlaLeuProHisProProAlaGlnProProProProGlnGlnPhePro 40
Db 98 GGACCCGGCTTGGCGGTCTCCGGGGGGCGCGGAGCC----- 139
Qy 41 GlnPheHisValLysSerGlyLeuGlnIleLysAsnAlaIleLeuAspTyrLys 60
Db 140 -----AAGAGTACGCAGTGCACGACGACTACCAG 169
Qy 61 ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLys 80
Db 170 TTGTCGAAGCAGGTGTGGCGCTGTGAACGCAAGTGTGGAGTCTTCCATCGG 229
Qy 81 ArgThrGlnGluLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaAArgGlu 100
Db 230 CGCACTGGACAGAGTGTGCCCTGGAAGCTCTGTATGACAGCCCCAAGCCCGCAGAG 289
Qy 101 ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr 120
Db 290 GTAGACCATCACTGGCAGGCTTCTGGCGGCCCATATTGCTGCACTCTGGATGTGTAT 349
Qy 121 GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly 140
Db 350 GAGAACATGCACCATGCCAAGCGTCTCTCATCATCATGGAATGCATGGAAGGTGGT 409
Qy 141 GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer 160
Db 410 GAGTTGTTACAGGAGTTCAGGAGCGTGGCGACGAGCTTCTACATGAGAGAGCTGCA 469
Qy 161 GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis 180
Db 470 GAGATAATGGGATATTGGCACTGCCATCCAGTTTCTGCACAGCCATAACATTGCCAC 529
Qy 181 ArgAspValLysProGluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeuLys 200
Db 530 CGAGATGTCAAGCCTGAAAACTTACTCTACACATCTAAGGAGAAAGACGAGTCTTAAG 589
Qy 201 LeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCys 220
Db 590 CTCACCGATTTTGGCTTTGTCAAGGAGACCAACC---CAAAATGCCCTCGACAGACCCCTGC 646
Qy 221 TyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys 240
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Db 647 TATACTCCCTATTATGTGGCCCTCGAGTCTCGGTCCAGAGAAATGATGACAGTCAATGT 706  
Qy 241 AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuGlyTyrProProPheTyr 260  
Db 707 GACATGTGGTCCCTGGGTGTCTATCATGTATCATCTCTCTTTGTGGCTTCCCAACCTTCTAC 766  
Qy 261 SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr 280  
Db 767 TCCAAACAGGCGCCAGGCCATCTCCCGGGGATGAAGAGGAGGATTCGCTGGGCCAGTAC 826  
Qy 281 GluPheProAsnProGluTrpSerGluValSerGluGluValLysMetLeuIleArgAsn 300  
Db 827 GCCTTCCCAATCTGAGTGTCTCAGAGTCTCTCAGGATGCCAAGCAGCTGATCCGCCTC 886  
Qy 301 LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTrp 320  
Db 887 CTGTTGAAGACAGACCCCAAGAGAGGCTGACCATCTCACTGATTCATGAACCAACCCCTGG 946  
Qy 321 IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGlu 340  
Db 947 ATCAACCAATCATGTGTAGTGTCCACAGACCCCACTCCACAGCGCCGAGTGTCTGACGAG 1006  
Qy 341 AspLysGluArgTrpGluAspValLysGluGluMetThrSerAlaLeuAla-ThrMetAr 360  
Db 1007 GACAAAGACCACTGGGACGAAGTCAAGGAGGAGATGACCACT-----GCCCACTATGCG 1060  
Qy 360 gValAspTyrGluGlnIleLysLysLysLys-----IleGluAspAlaSerAsnProLe 378  
Db 1061 GGTAGACTACACAGGAGGATCAAGGA-CTTGGGCTGAAGACCTCTAACAACCGGCT 1119  
Qy 378 uLeuLeuLysArgArgLysLysAlaArgAlaLeuGluAlaAlaAla 393  
Db 1120 CCTCAACAGAGGAGAAAAAGAGGAGGAGGAGGAGCTCTCTGCTCCCTCA 1165

## RESULT 7

US-09-880-107-2146  
; Sequence 2146, Application US/09880107  
; Patent No. 6974667  
; GENERAL INFORMATION:  
; APPLICANT: Horne, Darci T.  
; APPLICANT: Vockley, Joseph G.  
; APPLICANT: Scherf, Uwe  
; APPLICANT: Gene Logic, Inc.  
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer  
; FILE REFERENCE: 44921-5028-WO  
; CURRENT APPLICATION NUMBER: US/09/880,107  
; CURRENT FILING DATE: 2001-06-14  
; PRIOR APPLICATION NUMBER: US 60/211,379  
; PRIOR FILING DATE: 2000-06-14  
; PRIOR APPLICATION NUMBER: US 60/237,054  
; PRIOR FILING DATE: 2000-10-02  
; NUMBER OF SEQ ID NOS: 3950  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 2146  
; LENGTH: 3061  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Genbank Accession No. 6974667 L07597  
US-09-880-107-2146

## Alignment Scores:

Pred. No.:	1.22e-40	Length:	3061
Score:	540.00	Matches:	138
Percent Similarity:	52.6%	Conservative:	77
Best Local Similarity:	33.7%	Mismatches:	139
Query Match:	25.6%	Indels:	56
DB:	4	Gaps:	16

US-10-469-221-2 (1-396) x US-09-880-107-2146 (1-3061)

Qy 15 ProProGlnProProThrProAlaLeuProHis-----ProProAlaGlnProPro 32

Db 1104 CCAGATTACGTCCCGCAGACACCAGGATTCCCGCAGCATCCCGCCAGCGCTGGGSCCC 1163  
Qy 33 -----ProProPro----- 35  
Db 1164 ATCAGCTGTTCCGGGGCTTCAGCTTCGTGGCCACCGCTTGTATGGAGACAGCGGCAAGC 1223  
Qy 36 -----ProGlnGlnPheProGlnPheHisValLysSerGlyLeuGlnIleLysLysAsn 53  
Db 1224 CTGCTGCCCG-CAGGCACCCCTGCACCTCGTGGTACAGCAACTCCAT---GGGAAGAAC 1279  
Qy 54 AlaIleIleAspAspTyrLysValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLys 73  
Db 1280 CTGCTTTTGTAGTCAGCGCTAGCTGTTAAAGAGACAAATGCTGGTGGGCTCCTACTCTGAG 1339  
Qy 74 ValLeuGlnIlePheAsnLysArgThrGlnGluLysPheAlaLeuLysMetLeuGlnAsp 93  
Db 1340 TGCAAGCGCTGTCTCCACAAGGCCACCAACATCGAGTATGCTGTCAAGGTCAATTGAT--- 1396  
Qy 94 CysProLysAlaArgArg-----GluValGluLeuHisTrpArgAlaSerGln 109  
Db 1397 -----AAGAGCAAGCGGATCCTTCAGAGAGATTGAGATTCTTCTGCGGTATGGCCAG 1450  
Qy 110 CysProHisIleValArgIleValAspValTyrGluAsnLeuTyrAlaGlyArgLysCys 129  
Db 1451 CACCCCAACATCATCACTCTGAAAAGATGTGTATGATGAT-----GGCAAAACAC 1498  
Qy 130 LeuLeuIleValMetGluCysLeuAspGlyGlyGluLeuPheSerArgIleGlnAspArg 149  
Db 1499 GTGTACTGTGTACAGAGCTGATCGCGGGTGGGAGCTGCTGCACAGATCTCTGCGCGCAG 1558  
Qy 150 GlyAspGlnAlaPheThrGluArgGluAlaSerGluIleMetLysSerIleGlyGluAla 169  
Db 1559 -----AAGTTCTTCTCAGAGCGGGAGCCAGCTTGTCTGCACACCATTTGCCAAACT 1612  
Qy 170 IleGlnTyrLeuHisSerIleAsnIleAlaHisArgAspValLysProGluAsnLeuLeu 189  
Db 1613 GTGGAGTATCTGCACCTCACAGGGGGTGTGTACAGGAGCCTGAAGCCAGCAACATCCTG 1672  
Qy 190 TyrThrSerLysArgProAsn---AlaIleLeuLysLeuThrAspPheGlyPheAlaLys 208  
Db 1673 TATGTGACGAGTCCGGGAATCCCGAGTGCCTCGCATCTGTGACTTGTGTTTGTCCAAA 1732  
Qy 209 GluThrThrSerHisAsnSer---LeuThrThrProCysTyrThrProTyrTyrValAla 227  
Db 1733 CAGCTGGGGCTGAGATGGCTCTTCATCACACCTTGTACACGCCAATTTTGTGGCG 1792  
Qy 228 ProGluValLeuGlyProGluLysTyrAspLysSerCysAspMetTrpSerLeuGlyVal 247  
Db 1793 CTTGAGTGTGAAAGCGCCAGGCTACGATGAAGGCTGCACATCTGGAGCCTGGGCATT 1852  
Qy 248 IleMetTyrIleLeuLeuCysGlyTyrProPheTyrSerAsnHisGlyLeuAlaIle 267  
Db 1853 CTGCTGTACACCATGCTGGCAGATATACCTCAATT-----GCCAAGCTCCAGGTAC 1906  
Qy 268 SerPro---GlyMetLysThrArgIleArgMetGlyGlnTyrGluPheProAsnProGlu 286  
Db 1907 ACACAGAGGAATCTTAACCCGATCGGCAGTGGGAGTTTACCCTCAGTGGGGGAAT 1966  
Qy 287 TrpSerGluValSerGluGluValLysMetLeuIleArgAsnLeuLysThrGluPro 306  
Db 1967 TGGAACACAGTTTCAGAGACAGCAAGGACCTGGTGTCCAAAGATGTACACGTGGATCCC 2026  
Qy 307 ThrGlnArgMetThrIleThrGluPheMetAsnHisProTrpIleMetGlnSerThrLys 326  
Db 2027 CACACGCGCTCAGACTAAGCAGGTCTCTGACAGATCCATGGGTACCCCAAGAAAGCAAG 2086  
Qy 327 ValProGlnThrProLeu---HisThrSerArgValLeuLysGluAspLysGluArgTrp 345  
Db 2087 CTTCCCAAGCCAGCTGTCTCCACAGGACCTACAGCTT----- 2125  
Qy 346 GluAspValLysGluGluMetThrSerAlaLeuAlaThrMetArgValAspTyrGluGln 365

Db 2126 -----GTGAAGGAGGCGCATGGCTGCGCACACTCCGCACTCAACAGCTCAAGCCACC 2179  
Qy 366 IleLysIleLysLysIleGluAspAlaSerAsnProLeuLeuLeuLysArgArgLysLys 385  
Db 2180 CCCAGCTGAAGCCCATCGAGTCATCC-----ATCCTGGCCAGCGCGCA----- 2224  
Qy 386 AlaArgAlaLeuGluAlaAlaLeu 394  
Db 2225 GTGAGGAAGTTGCCATCCACACCCTG 2251

## RESULT 8

US-09-733-388-5

; Sequence 5, Application US/09733388  
; Patent No. 6602698  
; GENERAL INFORMATION:  
; APPLICANT: Donoho, Greg  
; APPLICANT: Scoville, John  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Friedrich, Glenn  
; APPLICANT: Zambrowicz, Brian  
; APPLICANT: Abuin, Alejandro  
; APPLICANT: Sands, Arthur T.  
; TITLE OF INVENTION: No. 6602698el Human Kinase Proteins and  
; FILE REFERENCE: LEX-0103-USA  
; CURRENT APPLICATION NUMBER: US/09/733,388  
; CURRENT FILING DATE: 2000-12-07  
; PRIOR APPLICATION NUMBER: US 60/169,428  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 1671  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-733-388-5

## Alignment Scores:

Pred. No.: 1.21e-40 Length: 1671  
Score: 536.00 Matches: 135  
Percent Similarity: 53.0% Conservative: 75  
Best Local Similarity: 34.1% Mismatches: 145  
Query Match: 25.5% Indels: 41  
Gaps: 14

US-10-469-221-2 (1-396) x US-09-733-388-5 (1-1671)

Qy 2 GlnGlyGlnSerProValPro---PheProAlaProAlaProProGlnProPro 20  
Db 37 CAGCCGAGCGCGCGCATCCCGCGCCTCTGCGCGCGCGCGCGCGCGCGCGCG 96  
Qy 21 ThrProAlaLeuProHisProProAlaGlnProPro-----Pro 33  
Db 97 CTCGCCAGCGCG-----CGCCGCGCGCGCTCTCCGCGCGCGGGAAGTTGCGCGCGCGC 150  
Qy 34 ProPro-GlnGlnPheProGlnPheHisValLysSerClyLeuGlnLysLysAs 53  
Db 151 GAGCCGCTGCTGCGCCATGCGCGGAGAACCGCGGAGAGAGAGCTCTCTCGGAAAAAGCA 210  
Qy 53 nAlaIleIleAspAspTyrLysValThr-----SerGlnValLeuGlyLeuGly 70  
Db 211 AGCT-----GAGACATCAAGAGATCTTCGAGTTCAAGAGAGACCTCGGAACCGGGC 264  
Qy 70 eAsnGlyLysValLeuGlnIlePheAsnLysArgThrGlnGlnLysPheAlaLeuLysMe 90  
Db 265 CTTTTCCGAGTGGTTTTAGCTGAAGAGAGAGCACTGGCAAGCTCTTTGCTGTAAGTG 324  
Qy 90 tLeuGlnAspCysProLysAlaArgArgGluValGluLeuHis-----Tr 105  
Db 325 TATCCCTAAGAGCGCTGAAGGCGCAGGAAGAGCAGCATAGAGATGAGATGCGCTCT 384  
Qy 105 pArgAlaSerGlnCysProHisIleValArgIleValAspValTyrGluAsnLeuTyrAl 125

Db 385 GAGAAAGATTAAAGCATGAAATATTGTTGCCCTGGAGACATTTATGAAAGC----- 436  
Qy 125 aGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGlyGluLeuPheSerAr 145  
Db 437 ----CCAAATACCTTACTGTCATGAGCTGGTGTCTCGGTGGAGAGCTGTTGACCG 492  
Qy 145 gIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSerGluIleMetLysSe 165  
Db 493 GATAGTGGAGAGGGG-----TTTTATACAGAGAAGGATGCCAGCACTCTGTATCCGCCA 546  
Qy 165 rIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHisArgAspValLysPr 185  
Db 547 AGTCTTGGAGCGCGTGTACTTCTCCACAGAATGGCATCGTCCACAGAGACCTCAAGCC 606  
Qy 185 oGluAsnLeuLeuTyrThrSerLysArgProenAlaIleLeuLysLeuThrAspPheGl 205  
Db 607 CGAAAAATCTCTTGTACTACAGTCAAGATGAGGAGTCCAAAAATAATCATGACTTTGG 666  
Qy 205 yPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCysTyrThrProTyrTy 225  
Db 667 ATTGTCAAAAAATGGAGGGCAAGGAGATGTGATGTCCACTGCTGTGGAACTCCAGGCTA 726  
Qy 225 rValAlaProGluValLeuGlyProGluLysTyrAspLysSerCysAspMetTrpSerLe 245  
Db 727 TGTCTGCTCTGAAGTCTCTGCCCCAGAAACCTTACAGCAAAAGCGTTGACTGTGTTCCAT 786  
Qy 245 uGlyValIleMetTyrIleLeuLeuCysGlyTyrProProPheTyrSerAsnHisGlyLe 265  
Db 787 CGGAGTGATTGCTTACATCTTGTCTGCGGCTACCTCTCTTTTATGATGAAAAAT----- 841  
Qy 265 uAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyrGluPheProAsnPr 285  
Db 842 -----GACTCCAAGCTCTTTGAGCAGATCTCAAGGGCGGAATATAGATTGACTCTCC 894  
Qy 285 oGluTrpSerGluValSerGluGluValLysMetLeuIleArgAsnLeuLysThrGl 305  
Db 895 CTACTGGGATGACATCTCCGACTCTGCAAAAGACTTTCATTTCGGAACCTGATGAGAAGGA 954  
Qy 305 uProThrGlnArgMetThrIleThrGluPheMetAsnHisProTrpIleMetGlnSerTh 325  
Db 955 CCCGAATAAAGATACACGTGTGAGCAGCGAGCTCGGCACCCCATGGATCGCTGGTGACAC 1014  
Qy 325 rLysValProGlnThrProLeuHisThrSer-----ArgValLeuLysGlu---As 341  
Db 1015 AGCCCTCAACAAAAAC---ATCCACGAGTCCGTGAGCGCCAGATCCGGAACAACTTTCG 1071  
Qy 341 pLysGluArgTrpGluAspValLysGluGluMetThrSerAlaLeuAlaThrMetArgVa 361  
Db 1072 CAAGAGCAAAATGG-----AGACAAAGCATTTAATGCCACGCGCGCTCGTGAGA-- 1117  
Qy 361 lAspTyrGluGlnIleLysIleLysLysIleGluAspAlaSerAsn 376  
Db 1118 -CATATGAGAAAACTACCTCGCGCAGCGCTGGAGAGTTCAAT 1162

## RESULT 9

US-10-446-175-5

; Sequence 5, Application US/10446175  
; Patent No. 6806073  
; GENERAL INFORMATION:  
; APPLICANT: Donoho, Greg  
; APPLICANT: Scoville, John  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Friedrich, Glenn  
; APPLICANT: Zambrowicz, Brian  
; APPLICANT: Abuin, Alejandro  
; APPLICANT: Sands, Arthur T.  
; TITLE OF INVENTION: No. 6806073el Human Kinase Proteins and  
; FILE REFERENCE: LEX-0103-USA  
; CURRENT APPLICATION NUMBER: US/10/446,175  
; CURRENT FILING DATE: 2003-05-27  
; PRIOR APPLICATION NUMBER: US/09/733,388  
; PRIOR FILING DATE: 2000-12-07

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; PRIOR APPLICATION NUMBER: US 60/169,428
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1671
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-446-175-5

Alignment Scores:
Pred. No.: 1,21e-40 Length: 1671
Score: 536.00 Matches: 135
Percent Similarity: 53.0% Conservative: 75
Best Local Similarity: 34.1% Mismatches: 145
Query Match: 25.5% Indels: 41
DB: 3 Gaps: 14

US-10-469-221-2 (1-396) x US-10-446-175-5 (1-1671)

Qy 2 GlnGlyGlnSerProProValPro---PheProAlaProAlaProProGlnProPro 20
Db 37 CAGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCG 96
Qy 21 ThrProAlaLeuProHisProProAlaGlnProPro-----Pro 33
Db 97 CTCCCAGCGCG-----CCCCCGCGCGCTCTCCGCGCGGGAAGTTGCGCCGAGCCC 150
Qy 34 ProPro-ProGlnGlnPheProGlnPheHisValLysSerGlyLeuGlnLeuLysLysAs 53
Db 151 GAGCCGCGTCGTCGCCATGCGCCGCGGAGACGCGGAGAGAGCTCTCTCTCGGAAAAAGCA 210
Qy 53 nAlaIleIleAspAspTyrLysValThr-----SerGlnValLeuGlyLeuGlyI 70
Db 211 AGCT-----GAGACATCAAGAGAGATCTTCGAGTCAAGAGACCTCGGAGCCGCGGC 264
Qy 70 eAsnGlyLysValLeuGlnLeuPheAsnLysArgThrGlnGlnLysPheAlaLeuLysMe 90
Db 265 CTTTTCGGAAGTGGTTTGTAGTGAAGAGAGGCACTGGCAAGCTCTTCTGTGAAGTG 324
Qy 90 tLeuGlnAspCysProLysAlaArgArgGluValGluLeuHis-----Tr 105
Db 325 TATCCCTTAAGAAGCGCTGAAGGCGCAAGAGAGAGATAGAGATAGAGATAGCGCTCT 384
Qy 105 pArgAlaSerGlnCysProHisIleValArgIleValAspValTyrGluAsnLeuTyrAl 125
Db 385 GAGAAAGATTAAAGTGAATATTTGTTCCTCGAAGACATTTATGAAGC----- 436
Qy 125 aGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGlyLeuLeuPheSerAr 145
Db 437 -----CCAATCACCTGTACTTGGTTCATGCAGCTGGTCCGGTGGAGAGCTGTTGACCG 492
Qy 145 gIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSerGluIleMetLysSe 165
Db 493 GATAGTGGAGAAAGGG-----TTTATACAGAGAGAGATGCCAGCACTCTGATCCGCCA 546
Qy 165 rIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHisAspAspValLysPr 185
Db 547 AGTCTTGAGCGCGCTGACTATCTCCAGATGGGCATCGTCCACAGAGACCTCAAGCC 606
Qy 185 oGluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeuLysLeuThrAspPheG1 205
Db 607 CGAAATCTCTGTACTACAGTCAAGATGAGGATGCCAAATAATGATGACTGACTTTGG 666
Qy 205 yPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCysTyrThrProTyrTy 225
Db 667 ATTGTCAAAAATGAGGCGCAAAAGAGATGTGATGTCCCACTGCTGTGGAACTCCAGCCTA 726
Qy 225 rValAlaProGluValLeuGlyProGluLysTyrAspLysSerCysAspMetTrpSerLe 245
Db 727 TGTGCTCTCTGAAGTCTCTGCCCGCAAGAACCTTACGAAAGCGCTTCACTGCTGCTCAT 786
Qy 245 uGlyValIleMetTyrIleLeuLeuCysGlyTyrProProPheTyrSerAsnHisGlyLe 265

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Db 787 CGGAGTATTCCTACATCTTCTCGCGGTACCTCTCTTTATGATGAAAT----- 841
Qy 265 uAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyrGluPheProAsnPr 285
Db 842 -----GACTCCAAGCTCTTTGAGCAGATCCTCAAGCGGGAATATGAGTTTGACTCTCC 894
Qy 285 oGluTrpSerGluValSerGluGluValLysMetLeuIleArgAsnLeuLysThrG1 305
Db 895 CTACTGGGATGACATCTCCGACTCTGCAAAAGACTTCATTCCGGAACCTGATGGAGAGGA 954
Qy 305 uProThrGlnArgMetThrIleThrGluPheMetAsnHisProTrpIleMetGlnSerTh 325
Db 955 CCGAATAAAGATACACAGCTGTGAGCAGCGAGCTCGGCCACCCATGGATCGCTGTGACAC 1014
Qy 325 rLysValProGlnThrProLeuHisThrSer-----ArgValLeuLysGlu---As 341
Db 1015 AGCCCTCAACAAAAAC---ATCCACGAGTCCGTCAGCGCCGAGATCCGGAACAACTTTCG 1071
Qy 341 pLysGluArgTrpGluAspValLysGluGluMetThrSerAlaLeuAlaThrMetArgVa 361
Db 1072 CAGAGCAATAGG-----AGACAAGCATTTATGCCACGCGCTCGTGAGAGA-- 1117
Qy 361 lAspTyrGluGlnIleLysIleLysLysIleGluAspAlaSerAsn 376
Db 1118 -CATATGAGAAACTACACCTCGCGCAGCAGCTGGACAGTCAAAT 1162

RESULT 10
US-09-620-312D-526
; Sequence 526, Application US/09620312D
; Patent No. 659662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunding
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghaast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 659662el Nucleic Acids and
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 526
; LENGTH: 1733
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (215) ..(1372)
US-09-620-312D-526

Alignment Scores:
Pred. No.: 2,72e-40 Length: 1733
Score: 532.50 Matches: 134
Percent Similarity: 53.4% Conservative: 73

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Qy 122 AsnLeuTyrAlaGlyArgLysCysLeuLeuLeuValMetGluCysLeuAspGlyGlu 141  
Db 510 AGC-----CCAAATCACCTCTACCTGGTGCATGCACTGTCTGTGGTGAGAA 557  
Qy 142 LeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSerGlu 161  
Db 558 CTCCTCGATCGATAGTGGAGAGGG-----TTTACACAGAGAAAGATGCCAGCACT 611  
Qy 162 IleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHisArg 181  
Db 612 CTCATCCGCCAGGTCCTGGATCGCGTACTATCTCCACAGAAATGGGCAATGTCCACAGG 671  
Qy 182 AspValLysProGluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeuLysLeu 201  
Db 672 GACCTCAAGCCGAGAAATCTCTTATCTACAGTCAAGACGAGGAGTCCAAATAATATGATC 731  
Qy 202 ThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCysTyr 221  
Db 732 AGTGACTTTGGCTTGTGCAAAATGGAGGCAAGAGATGTGTCCACGGCTGCGGG 791  
Qy 222 ThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCysAsp 241  
Db 792 ACCCAGGCTATGTCTCCGAGTCTCCGAGAGTCTCCGAGAGAACCTACAGCAAGCTGTGGAC 851  
Qy 242 MetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProPheTyrSer 261  
Db 852 TGCTGGTCCATCGGGTGATCGCTATATCTTGTCTGTGTGTACCTCTCTTTTATGAT 911  
Qy 262 AsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyrGlu 281  
Db 912 GAAAT-----GACTCGAAGCTGTTTGAACAGATCCTCAAGGCAGAAATATGAG 959  
Qy 282 PheProAsnProGluTrpSerGluValSerGluValLysMetLeuIleArgAsnLeu 301  
Db 960 TTTGATCCCTACTGGGATGATCTCCGACTCTCCCAAGACTCTCAITTCGGAATCTG 1019  
Qy 302 LeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTrpIle 321  
Db 1020 ATGAGAGAAAGACCAATAAAGATACACTTGTGAGCAGGCGAGCTCGACACCCATGGATT 1079  
Qy 322 MetGlnSerThrLysValProGlnThrProLeuHisThrSer-----ArgValLeu 338  
Db 1080 GCTGGTGACACAGCCCTTAGCAAAAC---ATTCACGAATCTGTCAAGTCCAGATCCGG 1136  
Qy 339 LysGlu---AspLysGluArgTyrGluAspValLysGluGluMetThrSerAlaLeuAla 357  
Db 1137 AAGAAATTTGCAAGACCAATGG-----AGACAAGCGTTTAACGCCACCGCA 1184  
Qy 358 ThrMetArgValAspTyrGluGlnIleLysIleLysLysIleGluAspAlaSerAsn 376  
Db 1185 GTCGTGAGA---CATATGCGGAGGCTCCAGCTTGGCAGCAGCCTGGACAGTTCAAT 1238

## RESULT 12

US-10-355-975A-3  
; Sequence 3, Application US/10355975A  
; Patent No. 6759223  
; GENERAL INFORMATION:  
; APPLICANT: Immunex Corporation  
; APPLICANT: Bird, Timothy A.  
; APPLICANT: Virca, G. Duke  
; APPLICANT: Martin, Unja  
; APPLICANT: Anderson, Dirk M.  
; TITLE OF INVENTION: CALCIUM/CALMODULIN-DEPENDENT KINASE  
; FILE REFERENCE: 2923-B  
; CURRENT APPLICATION NUMBER: US/10/355.975A  
; CURRENT FILING DATE: 2003-01-30  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 1694  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-355-975A-3

Alignment Scores:  
Pred. No.: 5,03e-40 Length: 1694  
Score: 529.50 Matches: 136  
Percent Similarity: 51.9% Conservative: 71  
Best Local Similarity: 34.1% Mismatches: 138  
Query Match: 25.1% Indels: 56  
DB: 3 Gaps: 13

US-10-469-221-2 (1-396) x US-10-355-975A-3 (1-1694)

Qy 9 ProPheProAlaProAlaProProGlnProProThrProAlaLeuProHisProPro 28  
Db 113 CCCGAGGCTCCCTCGCGCTCCGATCCTCCGCTCCGATCCGCGCGCGGCGATCCCGCG 172  
Qy 29 AlaGlnProProProProGlnGlnPhePheHisValLysSerGlyLeu 48  
Db 173 ---GAGCCCGCGCGCG-CTTCCGCGCGCCCTTCCCGAGCG-CAACCCCTCGCGCGCCTA 227  
Qy 49 Gln----- 49  
Db 228 CAGCATTAGTCTCCATGGCCCGGAGAACGGCGAGAGCAGCTCCTCTCGAAAAAGCAA 287  
Qy 50 -----IleLysLysAsnAlaIleIleAspAspTyrLysValThrSerGlnValLeu 66  
Db 288 GCAGAGACATTAAGAA-----ATCTCGAGTTCAAGGAGACC-----CTC 329  
Qy 67 GlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLysArgThrGlnGluLysPhe 86  
Db 330 GGAACCTGGGCGCTTTCTGAAGTTGTTTAGCCGAGAGAAAGCTACTGGGAAGCTCTTC 389  
Qy 87 AlaLeuLysMetLeuGlnAspCysProLysAlaArgGluValGluLeuHis----- 104  
Db 390 GCAGTGAAGTGCATCCCGAGAGAGGCGCTGAGGGCAAGGAGGAGCAGCAGCAGAACGAG 449  
Qy 105 -----TrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyrGlu 121  
Db 450 ATTGCGCTGTGTAGAAAGATTAAGACATGAAACATTTGCTTGTGGAAGATATTATGAA 509  
Qy 122 AsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGlu 141  
Db 510 AGC-----CCAAATCACCTCTACCTGTGTATGCACTTGTCTGTGGTGAGAA 557  
Qy 142 LeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSerGlu 161  
Db 558 CTCTTCGATCGATAGTGGAGAGGG-----TTTACACAGAGAAAGATGCCAGCACT 611  
Qy 162 IleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHisArg 181  
Db 612 CTCATCCGCGAGTCTCGATGCGTATATCTCCACAGAAATGGGCAATGTCTCCACAGG 671  
Qy 182 AspValLysProGluAsnLeuTyrThrSerLysArgProAsnAlaIleLeuLysLeu 201  
Db 672 GACCTCAAGCCGAGAAATCTTATCTACAGTCAAGACGAGGAGTCCAAATAATATGATC 731  
Qy 202 ThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCysTyr 221  
Db 732 AGTGACTTTGGCTTGTGCAAAATGGAGGCAAGAGATGTGTCTCCAGCGCTGCGGG 791  
Qy 222 ThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCysAsp 241  
Db 792 ACCCGAGGCTATGTGTCTCGGAAAGTTCTCGCGCAAGAACCGTACAGCAAGCTGTGGAC 851  
Qy 242 MetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProPheTyrSer 261  
Db 852 TGCTGGTCCATCGGGTGATCGCGTATATCTTGTGTGTGTACCTCTCTTTTATGAT 911  
Qy 262 AsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyrGlu 281  
Db 912 GAAAT-----GACTCGAAGCTGTTTGAACAGATCCTCAAGGCAGAAATATGAG 959  
Qy 282 PheProAsnProGluTrpSerGluValSerGluValLysMetLeuIleArgAsnLeu 301  
Db 960 TTTGATCCCTACTGGGATGATCTCCGACTCTCCCAAGACTCTCAITTCGGAATCTG 1019



Db 810 AAATCTTTT-----GACAGATTGTGAAGCGCAGTAGTCAGATTGACTCTCT 857

Qy 286 GlutPserGluValSerGluGluValLysMetLeulleArgAsnLeuLeuLysThrGlu 305  
||| : : : : :  
858 TACTGGAGCACACTCTGACTCTGCCAAAGATTTCATCCGCCTTGATGAGAAGGAC 917  
||| : : : : :  
306 ProThrGlnArgMetThrIleThrGluPheMetAsnHisProTrpIleMetGlnSerThr 325  
||| : : : : :  
918 CCAGAAAAAAGATTCACTGTGTGAGCAGGCCTTGACAGCACCCTCATGGATTGCGAGGATACA 977  
||| : : : : :  
326 LysValProGlnThrProLeuHis-----ThrSerArgValLeuLysGluAsp----- 341  
||| : : : : :  
978 GCTCTAGATAAGAT--ATCCACAGTCGGTGAGTGAGCAGATCAAGAAGAACCTTTGCC 1034  
||| : : : : :  
342 LysGluArgTrpGluAspValLysGluGluMetThrSerAlaLeuAlaThrMetArg 360  
||| : : : : :  
1035 AAGAGCAAGTGG-----AAGCAACCTTCAATGCCACGGCTGTGGTGGG 1079  
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RESULT 15  
US-09-949-016-1591  
; Sequence 1591, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 20/012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1591  
; LENGTH: 1442  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-1591

Alignment Scores:  
Pred. No.: 1.63e-39 Length: 1442  
Score: 523.00 Matches: 125  
Percent Similarity: 54.3% Conservative: 70  
Best Local Similarity: 34.8% Mismatches: 126  
Query Match: 24.8% Indels: 38  
DB: Gaps: 11

US-10-469-221-2 (1-396) x US-09-949-016-1591 (1-1442)

Qy 18 GlnProProThrProAlaLeuProHisProProAlaGlnProProProProGln 37  
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||| : : : : :  
Qy 38 GlnPheProGlnPheHisValLysSerGlyLeuGlnIleLysValLysAlaIleasp 57  
||||| : : : : :  
Db 129 CAGTGGGCCATGTCTGGGGGAGTGGAGGGCCCCCAGGTGGAGAGCGGGAGGACATTAGA 188  
||| : : : : :  
Qy 58 AspTyrLysValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIle 77  
||||| : : : : :  
Db 189 GACATCTACGACTCCGAGATGTTCTGGGCACGGGGCCCTTCGAGGTGATCTCGSCA 248  
||| : : : : :  
Qy 78 PheAsnLysArgThrGlnGluLysPheAlaLeuLysMetLeuGlnAspCysProLysAla 97  
||| : : : : :  
Db 249 GAAGATAAGAGGACGCAAGAGCTGTGGCCATCAATGCATT-----GCC 293  
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Qy 98 ArgArgGluValGlu-----LeuHistrip 105  
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Db 294 AAGAGGCCCTGGAGGGCAAGGAGGACGATGGAGATGAGATTGCTGCTCTGCAC---- 350  
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Search completed: June 19, 2006, 17:37:21  
Job time : 255 secs



GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2006, 16:04:24 ; Search time 261 seconds  
(without alignments)  
8538.278 Million cell updates/sec

Title: US-10-469-221-1  
Perfect score: 1191  
Sequence: 1 tccagggcagagccgc.....ctgggtctggccactga 1191

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 93554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA.\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/ina/1 COMB.seq.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/ina/5 COMB.seq.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6A COMB.seq.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6B COMB.seq.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/ina/7 COMB.seq.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/ina/H COMB.seq.\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PCTUS COMB.seq.\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PP COMB.seq.\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/ina/RE COMB.seq.\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/backfiles.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1181.4	99.2	1336	3	US-09-023-655-1397
2	1048.4	88.0	2258	3	US-09-016-434-1415
3	555.8	46.7	2481	3	US-09-016-434-1088
4	555.8	46.7	2481	3	US-09-016-434-1088
5	555.8	46.7	2509	3	US-09-949-016-5682
6	528.44	3	1333	3	US-09-142-551A-1
7	142.2	11.9	438	4	US-09-880-107-810
8	126.4	10.6	1442	3	US-09-949-016-1590
9	126.4	10.6	1442	3	US-09-949-016-1591
10	122.6	10.3	1694	3	US-09-579-664B-3
11	122.6	10.3	1694	3	US-10-355-975A-3
12	122.6	10.3	1694	5	US-09-980-464-3
13	122.2	10.3	1480	3	US-09-016-434-1454
14	120.4	10.1	1282	2	US-08-878-989-12
15	120.4	10.1	1282	3	US-09-272-796-12
16	120.4	10.1	1282	3	US-09-016-434-953
17	120.4	10.1	1584	3	US-09-789-451-205
18	117.8	9.9	1458	3	US-09-230-896C-5
19	111	9.3	1733	3	US-09-620-312D-526
20	109.8	9.2	1074	3	US-09-733-388-3
21	109.8	9.2	1074	3	US-10-446-175-3
22	109.8	9.2	1158	3	US-09-733-388-1
23	109.8	9.2	1158	3	US-10-446-175-1

ALIGNMENTS

RESULT 1  
US-09-023-655-1397  
; Sequence 1397, Application US/09023655  
; Patent No. 6607879  
; GENERAL INFORMATION:  
; APPLICANT: Cocks, Benjamin G.  
; APPLICANT: Susan G. Stuart  
; APPLICANT: Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
; TITLE OF INVENTION: EXPRESSION  
; NUMBER OF SEQUENCES: 1508  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/023,655  
; FILING DATE: HEREWITH  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0001 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 1397:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1336 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GENBANK

fdw  
3/19/03

Sequence 5, Appli  
Sequence 5, Appli  
Sequence 2, Appli  
Sequence 1, Appli  
Sequence 2146, Ap  
Sequence 5449, Ap  
Sequence 41, Appl  
Sequence 3371, Ap  
Sequence 1, Appli  
Sequence 1, Appli  
Sequence 6, Appli  
Sequence 10, Appli  
Sequence 1, Appli  
Sequence 4, Appli  
Sequence 4, Appli  
Sequence 5, Appli  
Sequence 5, Appli  
Sequence 58, Appli  
Sequence 20, Appli  
Sequence 20, Appli









Qy	500	GTGAGGCCATCCAGTATCTCGATCTCAATCAACATTTGCCCATCGGGATGTCAAGCCTGAGA	559
Db	489	GCATCGCATCCAGTTTTCTGCACAGCCATCAACATTTGCCACCGAGATGTCAAGCCTGAAA	548
Qy	560	ATCTCTTATACACCTCCAAAAGGCCAACGCCATCTGTAAACTCCTGAAACTCCTGAACTTTGGCTTTG	619
Db	549	ACCTACTCTTACACATCTTAAGGAGNAAGACGAGTGCTTTAAGCTCACCGATTTTGGCTTTG	608
Qy	620	CCAAGGAAACCAACAGCCCAAACTCTTTTGACCACTCTCTTGTATTACACCGTACTATGTGG	679
Db	609	CTAAGGAGAGCCAC---CCAAAAATGCCCTTGACAGACACCGCTGTACTCTCCCTATTATGTGG	665
Qy	680	CTCCAGAAAGTCTGGGTCGAGAGAAAGTATGACAAAGTCTGTGACATGTGTCCTCGGTG	739
Db	666	CCCCCTGAGGTCCTGGGTCGAGAGAAAGTATGACAAAGTCAATGTGACATGTGTCCTCGGTG	725
Qy	740	TCATCATGTATACATCTCTGTGTGGGTATCCCCCTTTCTACTCCAAACCGGCTTTGCCA	799
Db	726	TCATCATGTATACATCTCTCTTTGTGGCTTCCACCGCTTTCTACTCCAAACCGGGCCAGGCCA	785
Qy	800	TCTCTCCGGGCATGAAGACTCGCATCCGAATGGCCAGTATGAATTTCCCAACCCAGAAT	859
Db	786	TCTCCCCGGGGATGAAGAGGAGGATTCGCTTGGGCCAGTAGCGGCTTCCCAATCCTGAGT	845
Qy	860	GGTCAGAAGTATCAGAGGAAAGTGAAGATGTCTATTTCGGAATCTGCTGAAAACAGAGCCCA	919
Db	846	GGTCAGAAGTCTCTGAGGATGCCAAGCAGCTGATCCGCTCTCTTGAAGACAGACCCCA	905
Qy	920	CCGAGAAATGAACCATCACCGAGTTTATGAACACACCTTGGATCATGCAATCAACAAGG	979
Db	906	CAGAGAGGCTGACCATCACTCAGTTCATGAACCAACCCCTGGATCAACCAATCGATGTGATG	965
Qy	980	TCCCTCAAAACCCCACTGCACACAGCCGGGTCTCTGAAGGAGGACAAAGAGCGGTGGGAGG	1039
Db	966	TGCCACAGACCCCACTCCAACGCCCCGAGTGTCTGAGGAGGACAAAGACCACTGGGACG	1025
Qy	1040	ATGTCAAGAGGAGATGACCAAGTGCCTTTGGGCCACAATTCGCGGTTGACTACGACGAGATCA	1099
Db	1026	AAGTCAAGAGGAGATGACCAAGTGC-----CCACTATGCGGGTAGACTACGACCAAGTGA	1080
Qy	1100	AGATAAAAAAGATTG--AAGATGATCCAACCCCTCTGCTGAAGAGGGCGGAAGAACG	1157
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Qy	1158	TCGGGC	1163
Db	1141	GCAGGC	1146

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RESULT 7
US-09-880-107-810/c
; Sequence 810, Application US/09880107
; Patent No. 6974667
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherif, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 810
; LENGTH: 438
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

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; OTHER INFORMATION: Genbank Accession No. 6974667 AA400246
US-09-880-107-810

Query Match      11.9%; Score 142.2; DB 4; Length 438;
Best Local Similarity 98.0%; Pred. No. 1.1e-23;
Matches 144; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 438 AAGCTGGAATGACCACTGCTTGGCCACATGCGCTTGACTACGAGCAGATCAAGATA 379
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 1105 AAAAAGATTGAAGATGTCATCAACCCCTCTGCTGCTGAAGGCGGAGAAAGCTCGGCC 1164
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 378 AAAAAGATTGAAGATGTCATCAACCCCTCTGCTGCTGAAGGCGGAGAAAGCTCGGCC 319
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 1165 CTGGAGGCTGGCGCTCTGGCCCACTGA 1191
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 318 CTGGAGGCTGGCGCTCTGGCCCACTGA 292
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 8
US-09-949-016-1590
; Sequence 1590, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMERISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1590
; LENGTH: 1442
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1590

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2

**FEATURE:**

QY 363 GAATCTGTATCGCAGGAGAAAGTGCCTGCTGATTTGATGTCATGGAATGTTTGGACGGTGGAGA 422  
DB 383 TGACATCTATCAGAGTGGGGCCACCTCTACCTCATCATGAGTGTGTCGGGTGGGA 442  
QY 423 ACTCTTTAGCCGATCAGGATCAGGAGACGAGCATTTACAGAAAGAGAGCATCCGA 482  
DB 443 GCTCTTTGACCGTATTTGGAAAAAGGCTTCTA-----CACGGAGCGGACGCGCCG 496  
QY 483 AATCATGAAGAGCATCCGCTGAGGCGCATCCAGTATCTGCATTCATCAATCAACATTGCCCATCG 542  
DB 497 CCTCATCTTCAGGTGCTGATGCTGTAATACCTGATCATGCTGAGCATTTGACACCG 556  
QY 543 GGATGTCAAGCTCAGAAATCTTTATACACTCCAAAGAGCCCAACGCACTCTTGAACCT 602  
DB 557 GGATCTCAAGCCAGAAATCTGCTGTAATAAGCTTGGATGAGACTTCCAAATCATGAT 616  
QY 603 CACTGACTTTGGCTTTGCCAAGGAAACACACAGGACCCCGGCGAGTGTCTCTCCACCGCTGTGG 662  
DB 617 CTCGAGCTTTGGCTCTCCAAAGATGGAGGACCCCGGCGAGTGTCTCTCCACCGCTGTGG 676  
QY 663 TACACCGTACTATGCTGCTCCAGAAAGTGTGGTCCAGAGAAAGTATGACAAAGTCTCTGA 722  
DB 677 AACTCCGGGATGCTGGCCCTGAACTCTGAGTCTGAGGACCCCTACAGAAAGGCTGTGA 736  
QY 723 CATGTGCTCCGCTGCTATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 782  
DB 737 TTGCTGTCCATAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 796  
QY 783 CAACACCGCTTGGCATCTCTCCGGGCGATGAGACTCGCATCCGATGGGCCAGTATGA 842  
DB 797 CGAAGATGATGCCAACTCTTT-----GAAACAGATTTTGAAGGCCGAGTACGA 844  
QY 843 ATTTCCCAACCCAGAAATGCTCAGAAAGTATCAGAGAAAGTGAAGTGTCTCATTCGGAATCT 902  
DB 845 GTTTGACTCTCTTACTGAGACGACATCTGACTCTGCAAGATTTTCAATCCGGCACTT 904  
QY 903 GCTGAAAACAGAGCCCAACCCAGAGAAATGACCATCACCGAGTTTATGAACCAACCTTTGGAT 962  
DB 905 GATGGAAGGACCCAGAGAAAGATTCACCTGTGAGCAGGCTTGCAGCACCACCATGAT 964

## RESULT 9

US-09-949-016-1591  
; Sequence 1591, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1591  
; LENGTH: 1442  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-1591

Query Match 10.6%; Score 126.4; DB 3; Length 1442;  
Best Local Similarity 48.2%; Pred. No. 7.8e-20;  
Matches 463; Conservative 0; Mismatches 476; Indels 21; Gaps 3;

QY 6 GGGCCAGAGCCCGCGTGGCTTCCCG 65  
DB 23 GTGGCCAGGACGCGACGCGTGGAGGACCGGCGGCGACAGCTCGGCGCAACCAACCGCGGCG 82

QY 66 TGCCTCGCACCCCGCGCGAGCCGTT 125  
DB 83 CTCCAGCAGCCCGCGCGGAGCCCTTGGCTGTGGTGGGGGCGAGTGGGCGCATGCT 142  
QY 126 CCAGCTCAAGTCCGGCTTCAGATCAAGAAAGAGCGCATCATCGATCACTACAGGTGAC 185  
DB 143 GGGGCGAGTGGAAAGGCCCGCAGGTGGAAGCAGCGGAGGACATTAGACACATCTACGACTT 202  
QY 186 CAGCAGGTCTCGGGCTGGGCATCAACGGCAAGTTTTCAGATCTTCAACAAGAGAC 245  
DB 203 CCAGATGTTCTGGGACCGGGGCGCTTCTCGAGGTGATCTTGGCAGAAGATAGAGGAC 262  
QY 246 CCAGGAGAAATTCGCTCAAAATGCTTCAGGACTGCCCAAGCGCCGCGAGGAGGTGGA 305  
DB 263 GCAGAGCTGTGGCCATCAATGCAATGCAAGGAGGCGCTGGAGGCAAGGAGGAG 322  
QY 306 GCTGCACTGGCGG---GCTTCCAGTGCCTGCAATCGTACGGATCGTGGATGTGTACGA 362  
DB 323 CATGGAGATGAGATTGCTGCTGCACAAGATCAAGCACCCCAACATTGTAGCCCTGGA 382  
QY 363 GAATCTGTACGAGGAGGAGTGCCTGCTGATTTGATGATGATGATGATGATGATGATGATGAT 422  
DB 383 TGACATCTATGAGAGTGGGGGCCACCTCTACCTCATCATGACGCTGCTGCTGCTGCTGCTGCT 442  
QY 423 ACTCTTTAGCCGAAATCCAGGATCGAGGAGACCGGCAATTCACAGAAAGAGAGCATCCGA 482  
DB 443 GCTCTTTGACCGTATTTGGGAAAAGGCTTCTA-----CACGGAGCGGACGCGCGCG 496  
QY 483 AATCATGAAGAGCATCGTGGAGGCGCATCCAGTATCTGCAATTCATCAACATTTGCCCATCG 542  
DB 497 CCTCATCTTCAGGTGCTGATGCTGTGAAATACCTGCAATGCTGCGCATTTGACACCG 556  
QY 543 GGATGTCAAGCTGAGAAATCTTATACACTCCAAAGGCGCCCAACGCACTCTTGAACCT 602  
DB 557 GSATCTCAAGCCAGAGAAATCTGCTGCTACTACGCTGGATGAAAGACTTCCAAAATCATGAT 616  
QY 603 CACTGACTTTGGCTTTGCCAAGGAAACACACGAGCACAACCTTTGACCACTCTCTTCTGTTA 662  
DB 617 CTGAGCTTTGGCTCTCCAAAGATGAGGACCCGGGCGAGTGTGCTCTCCACCGCTGTGG 676  
QY 663 TACACCGTACTATGCTGCTCCAGAAAGTGTGGTCCAGAGAAAGTATGACAAAGTCTGTGA 722  
DB 677 AACTCCGGGATGCTGGCCCTGAACTCTGCTGCGCCAGAGCCCTACAGCAAGGCTGTGA 736  
QY 723 CATGTGCTCCGCTGCTCATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 782  
DB 737 TTGCTGTCCATAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 796  
QY 783 CAACCAAGGCTTGGCATCTCTCCGGGCGATGAGAGACTCGCATCCGATGGCGCGAGTATGA 842  
DB 797 CGAAGATGATGCCAACTCTTT-----GAAACAGATTTTGAAGGCCGAGTACGA 844  
QY 843 ATTTCCCAACCCAGAAATGCTCAGAAAGTATCAGAGAAAGTGAAGTGTCTCATTCGGAATCT 902  
DB 845 GTTTGACTCTCTTACTGAGACGACATCTGACTCTGCAAGATTTTCAATCCGGCACTT 904  
QY 903 GCTGAAAACAGAGCCCAACCCAGAGAAATGACCATCACCGAGTTTATGAACCAACCTTTGGAT 962  
DB 905 GATGGAAGGACCCAGAGAAAGATTCACCTGTGAGCAGGCTTGCAGCACCACCATGAT 964

## RESULT 10

US-09-579-664B-3  
; Sequence 3, Application US/09579664B  
; Patent No. 6514719  
; GENERAL INFORMATION:  
; APPLICANT: Immunex Corporation  
; APPLICANT: Bird, Timothy A.  
; APPLICANT: Virca, G. Duke  
; APPLICANT: Martin, Unja  
; APPLICANT: Anderson, Dirk M.  
; TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES





; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 1694  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-980-464-3

Query Match 10.3%; Score 122.6; DB 5; Length 1694;  
Best Local Similarity 52.7%; Pred. No. 6.4e-19;  
Matches 325; Conservative 0; Mismatches 274; Indels 18; Gaps 2;

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D 480 AACATTGTGCTTGGAGATATTATGAAGCCCAATACCTCTACCTGCTCATGCA 539
QY 406 TGTGTGACGCTGAGAACTCTTTAGCCGATCCAGATCGAGGACCGGATTCACA 465
D 540 CTTGTGCTGTGAGAACTCTTCGATCGGATAGTGGAGAGG-----GTTTACACA 593
QY 466 GAAAGAGAAGCATCCGAAATCATGAAGACATCGGTGAGGCCATCCAGTATCTCATTC 525
D 594 GAGAAAGATGCCACTCTCATCGCCAGGTCTGATGCCGTATATCTATCTCCAGA 653
QY 526 ATCAACATGTCCTGCGGATGTCAAGCTGAGAAATCTTTATACACTCCAAAGGCC 585
D 654 ATGGGCATTTGCCACAGGACCTCAAGCGGAGAAATCTTTATACAGTCAAGACGAG 713
QY 586 AACGCCATCTGAACTCACTGACTTTGGCTTTGCCAAGGAAACACACGACCACTCT 645
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QY 646 TTGACCACTCTCTTTATACACCGTACTATGTGCTCCAGAGTGTCTGGTCCAGAGAAG 705
D 774 ATGTCCAGGCTGCGGACCCAGGCTATGTTGCTCCGGAAGTCTCGCCAGAACCG 833
QY 706 TATGACAAGTCTGTGACATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 765
D 834 TACAGCAAGATGTGGACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 893
QY 766 TATCCCTCTCTTACTCCACACCGCTTGGCCATCTCTCGGCGCATGAGATCGCATC 825
D 894 TACCTCTCTTTTATGATGAAATGACT-----CGAAGCTGTTTGAACAGATC 941
QY 826 CGAATGGCCAGTATGAAATTTCCCAACCCAGAAATGCTCAGAAATATCAGAGGAAGTGAAG 885
D 942 CTCAGGCGAATATGATTTGATTTCCCTACTGGGATGACATCTCGACTCTGCCAAA 1001
QY 886 ATGCTCATTCGGAATCTGTGAAACAGAGCCCAACCCAGAGAATGACCATCACCGAGTTT 945
D 1002 GACTTCATTCCGAATCTGATGGAGAAAGACCCAAATAAAGATACACTTGTGAGCAGCA 1061
QY 946 ATGAACACCCCTTGGAT 962
D 1062 GCTCGACACCCCTGGAT 1078
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## RESULT 13

US-09-016-434-1454  
Sequence 1454, Application US/09016434  
Patent No. 6500938

## GENERAL INFORMATION:

APPLICANT: Janice Au-Young  
APPLICANT: Jeffrey J. Seilhamer  
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
NUMBER OF SEQUENCES: 1490  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 PORTER DRIVE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/016,434  
FILING DATE: HEREWITH  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, Karen J  
REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: PA-0002 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 1454:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1480 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GENBANK  
CLONE: g790789  
US-09-016-434-1454

Query Match 10.3%; Score 122.2; DB 3; Length 1480;  
Best Local Similarity 47.8%; Pred. No. 7.5e-19;  
Matches 460; Conservative 0; Mismatches 482; Indels 21; Gaps 3;

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QY 3 CCAGGCGCAGAGCCCGCGGTGCTTCCCGCCCGCGCCCGCCCGCGCAGAGTCCCGCAC 62
D 30 CCAGGCGCAGAGCCCGCGGTGAGGACCGCGCCCAACAGCCCGCGGCGCTC 89
QY 63 CCTGCTGCTGCGCACCCCCCGCGCGCGCGCGCGCGCGCGCGCGCAGAGTCCCGCA 122
D 90 CCAGGCGCAGCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCAT 149
QY 123 GTTCCACGTCAGTCCGCGCTGCAGATCAAGAAAGACGCCATCATCGATCAGTACAGGT 182
D 150 GCTGGGGGAGTGGAGAGGCCCGAGGTGGAGAGCAGCGCGGAGGACATTAGAGACATCTACA 209
QY 183 CACGACCGCAGGTCTCTGGGCTGGGCATCAACCGGCAAAAGTTTTCAGATCTTCAACAGAG 242
D 210 CTTCCGAGATGTTCTGGCAGCGGGGCTTCTCGAGGTGATCTCTGGCAGAGATGAAG 269
QY 243 GACCCAGGAGAAATTCGCTCTCAAAATGCTTCAGGACTGCGCCCAAGCGCGCGCGGAGGT 302
D 270 GACGCAAGAGCTGGTGGCCATCAAAATGCAATTCGCAAGAGGCGCTCGAGGCGCAAGAG 329
QY 303 GGAGCTGCAC---TGGCGGCGCTCCCGAGTCCCGCACATCGTACGATCGTGTGATGTA 359
D 330 CAGCATGGAGATGAGATTGCTGCTCTGCACAAGATCAAGCACCACCAATTTAGCCCT 389
QY 360 CGAGAAATCTGTACGCGAGGAGGAAGTGCCTGCTGATTTGTTCATGGAATGTTTGGACGGTGG 419
D 390 GGATGACATCTATGAGAGTGGGGCCACCTTACCTCATCATGTCAGTCTGCTGCGGTGG 449
QY 420 AGAATCTTTAGCGGAATCCAGATCGAGGACCGAGGATTCACAGAAAGAGAGCATC 479
D 450 GGAGCTCTTTGACCGGTATTTGTGAAAGAGGCTTCTA-----CACGCGCGGCGACCCAG 503
QY 480 CGAAATCATGAAGAGCATCGGTGAGGCCATCAGTATCTGCAATTCATCAATTCACCCCA 539
D 504 CGCCTCATCTTCCAGGTCTGTGATGCTGTGAATACCTGATGATGACCTGGGCAATGTACA 563
QY 540 TCGGGATGTCAAGCCTGAGAATCTCTTTATACACCTTCCAAAGGCCCAACGCCCATCTCGAA 599
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Db 564 CCGGATCTCAAGCAGAGAAATCTGCTACTACAGCTGGATGAAGACTTCAAAATCAT 623  
Qy 600 ACTCACTGACTTTGGCTTTGCCAAGAAACACACAGCCCAACTCTTTGACCACCTCTTG 659  
Db 624 GATCTCGACTTTGGCTCTCCAGATGGAGGACCCGGGCGAGTGCTCTCCACCGCTG 683  
Qy 660 TTATACACCTACTATGTGCTCCAGAGTGTGGTCCAGAGAAATGATGACAAGTCTTG 719  
Db 684 TGGAACTCCCGGATAGCTGGCCCTGAAAGTCTGGCCCAAGAGCCCTTACAGCAAGGCTGT 743  
Qy 720 TGACATGTGCTGGCTGCTCATGTATACATCTGCTGTGGGTATCCCCCTTCTA 779  
Db 744 GGAATGTGCTCATAGTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTA 803  
Qy 780 CTCAACACCGGCTTCCCACTCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTA 839  
Db 804 TGACGAGATGATGCCAACTCTT-----GAACAGATTTGAAGGCCGAGTA 851  
Qy 840 TGAATTTCCCAACCCAGAAATGGTCAGAAATGATGAGAGAAATGAAATGCTCATTTGGAA 899  
Db 852 CGAGTTTGACTCTCTTACTTGGGACGACATCTCTGACTCTGCCAAAGATTTTATCCGGCA 911  
Qy 900 TCTGCTGAACACAGAGCCACCCAGAGAAATGACCATCACCGAGTTTATGAACCAACCTTG 959  
Db 912 CTTGATGGAGAGACCCAGAGAAAGATTCACTGTGACGAGGCTTGACGACCCCATG 971  
Qy 960 GAT 962  
Db 972 GAT 974

RESULT 14  
US-08-878-989-12  
; Sequence 12, Application US/08878989  
; Patent No. 5885803  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Guegler, Karl G.  
; APPLICANT: Lal, Preeti  
; APPLICANT: Goli, Surya K.  
; APPLICANT: Shah, Purvi  
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN  
; TITLE OF INVENTION: KINASES  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/878,989  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J J  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0321 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; TELEX:

; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1282 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: PROSNOT06  
; CLONE: 827431  
; US-08-878-989-12  
  
Query Match 10.1%; Score 120.4; DB 2; Length 1282;  
Best Local Similarity 50.3%; Pred. No. 1.9e-18;  
Matches 416; Conservative 0; Mismatches 387; Indels 24; Gaps 4;  
  
Qy 142 CTGCAGATCAAGAAGAACGCCATCATCGATGACTACAAAGGTCAACAGGCTCACCAGCCAGGTCTCTGGGG 201  
Db 207 CTGCTGAAGAACAACACAGGAGGACATCAGCAGCGTCTACAGATCCCGAGAGGCTCGGC 266  
Qy 202 CTGGGATCAACGGCAAGTTTTCAGATCTTCAACAAGAGGACCCAGAGAAATTCGCC 261  
Db 267 TCGGGTGCCTTCTCCAGGTGGTGGCCCAAGGAGCGGGGCTCCGCACACCTCTGTGGCC 326  
Qy 262 CTCAA---AATGCTTCAGGACTGCCCAAGGCCCGCAGGAGGTGGAGCTGCATCTGCGG 318  
Db 327 CTCAGTGCATCCCAAGAGGCCCTCCGGGGCAAGAGGCCCTGTGGAGAACAGATC 386  
Qy 319 GCCTCCAGTGGCCGCACATCGTACGGATCGTGGATGTGTACGAGAAATCTGTACGAGGG 378  
Db 387 GCAGTCTCCGTAGGATCAGTCACCCCAACATCGTCTGAGGATGTCCACAGAGC 446  
Qy 379 AGGAAGTGCCTGATTTGTCATGGAATGTTGGACGGTGGAGAACTCTTTAGCCGAATC 438  
Db 447 CTTTCCCACTCTACCTGGCCATGGAACTGGTGACGGGTGGCGAGCTGTTTGACCGCATC 506  
Qy 439 CAGGATCGAGGAGACCCAGGCATTTACAGAAAGAGAGCATCCGAAATCATGAAGAGCATC 498  
Db 507 ATGGAGCGGG-----CTCCTACACAGAGAGGATGCCAGCATCTGGTGGGTCAAGTTC 560  
Qy 499 GGTGAGGCCATCCAGTATCTGCATTCATCAACATTCAGCATTCGGGATGTCAAGCTGAG 558  
Db 561 CTTTGGCGCGTCTCTTACCTGCACAGCTGGGGATCGTGACCGGACCTTCAAGCCCGAA 620  
Qy 559 AATCTCTTATACACTTCCAAAGGCCCAAGCCATCTGAAACTCACTGACTTTGCTTT 618  
Db 621 AACCTCTGTATGCCACGCCCTTTGAGGACTCGAAGATCATGCTCTCTGACTTTGACTC 680  
Qy 619 GCCAAGGAAACACACAGCCCAACTCTTTGACCACTCTTGTGTTTATACACCGTACTATGTG 678  
Db 681 TCCA---AAATCCAGGCTGGAAACATGCTAGGCACCGCTGTGGGACCCCTGGATATGTG 737  
Qy 679 GTTCCAGAGTGTGGGTCCAGAGAAATGATGACAGTCTCTGTGACATGTTGTTCCCTGGGT 738  
Db 738 GCCCCAGAGCTCTTGGAGCAGAAACCCCTAGCGGAAGGCCGTAGATGTGTGGGCTGGGC 797  
Qy 739 GTCATCATGTACATCTGCTGTGGGTATCCCGCTTCTACTCCAAACACAGCCCTTGCC 798  
Db 798 GTCATCTCTACATCTGCTGTGGGTATCCCGCTTCTTACACAGAGGACCCCTGAG 857  
Qy 799 ATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTATGAATTTCCCAACCCAGAA 858  
Db 858 CTCT-----TCAGCCAGATCTCTGAGGCCAGCTATGAGTTTGATCTTCTTCTTC 905  
Qy 859 TGGTCAGAGTATCAGAGGAGTGAAGATGCTCATTCGGAATCTGCTGAAACAGAGCCCC 918  
Db 906 TGGGATGACATCTCAGAAATCAGGCAAAAGACTTTTATTCGGCACCTTCTGGAGCGAGACCTT 965  
Qy 919 ACCCAGAGATGACCATCACCGAGTTTATGAACACCCCTTGGATCAT 965  
Db 966 CAGAAGAGGTTCACTTCCCAAGGCTTGGGGACCTTTGGATCTT 1012

US-09-272-796-12  
; Sequence 12, Application US/09272796  
; Patent No. 6207148  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Guegler, Karl G.  
; APPLICANT: Lal, Preeti  
; APPLICANT: Goli, Preeti  
; APPLICANT: Shah, Purvi  
; APPLICANT: Shah, Purvi  
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN  
; TITLE OF INVENTION: KINASES  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/272,796  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; PRIOR APPLICATION NUMBER: 08/878,989  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0321 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1282 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: PROSNOT06  
; CLONE: 827431  
; US-09-272-796-12

Query Match 10.1%; Score 120.4; DB 3; Length 1282;  
Best Local Similarity 50.3%; Pred. No. 1.9e-18;  
Matches 416; Conservative 0; Mismatches 387; Indels 24; Gaps 4;  
QY 142 CTGCAGATCAAGAGAACGCCATCATGACTACAGGTCACAGCCAGGTCCTCGGG 201  
DB 207 CTGCTGAAGAAACACACGAGGACATCAGAGCGTCTACGAGATCCGGAGAGCTCGC 266  
QY 202 CTGGGCATCAACGGCAAGTTTTCAGATCTTCAACAAGAGGACCCAGAGAAATTCGCC 261  
DB 267 TCGGGTGCCTTCTCCGAGGTGGTCTGCGCCAGGAGCGGGCTCCGCACACCTCGTGGCC 326  
QY 262 CTCAA---AATGCTTCAGGACTGCCCAAGCCCGAGGAGGTGGAGTGCATCGCGG 318  
DB 327 CTCAAAGTGCATCCCAAGAGGCCCTCGGGGCAAGGAGGCCCTGGGTGGAGACGAGATC 386  
QY 319 GCCTCCAGTGCCTCCGACATCGTACGAGTGTGTACGAGAAATCTGTACGAGGG 378  
DB 387 GCAGTGTCCGTAGATCAGTACCCCAACATCGTCTGTGGAGGATGCCACGAGC 446  
QY 379 AGGAAGTGCCTGTGATTTGTATGGAATGTTTGGACGGTGGAGAACTCTTTAGCCGAATC 438

DB 447 CCTTCCACCTCTACCTGGCCATGGAACTGTGTAGGGTGGCGAGCTTTTGACCCGATC 506  
QY 439 CAGGATCGAGAGACACAGGCATTACAGAAAGAGAGCATCCGAAATCATGAAGAGCATC 498  
DB 507 ATGGAGGCGG-----CTCCTACACAGAGAGGATGCCAGCCATCTGGTGGGTCAAGTTC 560  
QY 499 GGTGAGGCCATCCAGTATCTGCATTCAATCAACATGCCCATGCCGATGTCAAGCCTGAG 558  
DB 561 CTTGGCGCGTCTCTACCTGCACAGCGCTGGGGATCGTGCACCGGAGCTCAAGCCCGAA 620  
QY 559 AATCTCTTATACACTTCCAAAGGCCCAACGCCCATCTCTGAAACTCACTGACTTTGGCTTT 618  
DB 621 AACCTCTGTATGCCAGCCCTTTGAGGACTCGAAGATCATGCTCTGTGACTTTGGACTC 680  
QY 619 GCCAAGGAAACACAGCCAGCACAACTCTTTGACCACTCTTGTGTATACACCTACTATGTG 678  
DB 681 TCCA---AAATCCAGGCTGGGAACATGCTAGGCACCGCCTGTGGGACCCCTGGATATGTG 737  
QY 679 GCTCCAGAAGTGTGGGTCCAGAGAAATGATGACAAGTCTCTGTGACATGTGTCTCTGGGT 738  
DB 738 GCCCAGAGCTCTTGGAGCAGAAACCCCTACGGGAAGCCGTAGATGTGTGGCCCTTGGGC 797  
QY 739 GTCATCATGTATCTCTGTGTGGGTATCCGCCCTTCTACTCCAAACACAGGCTTGGC 798  
DB 798 GTCATCTCTACATCTCTGTGTGGGTACCCCTTCTACGACGAGAGCCCTGAG 857  
QY 799 ATCTCTCGGGCATGAAGACTCGCATCCGAATGGGCGAGTATGAATTTCCCAACCCAGAA 858  
DB 858 CTCT-----TCAGCCAGATCTGAGGGCCAGCTATGAGTTTGAATNTCTTTC 905  
QY 859 TGGTCAGAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAATCTGCTGAAACAGAGCCC 918  
DB 906 TGGATGACATCTCAGAAATCAGGCAAGACTTTTATCGCACCTTCTGGACCGAGACCTT 965  
QY 919 ACCCAGAGAAATGACCATCACCGAGTTTATGAACCAACCCCTTTGGATCAT 965  
DB 966 CAGAAGAGGTTTCACTGCCAACAGGCCCTTGGGGACCTTTTGGATCTT 1012

Search completed: June 19, 2006, 18:07:05  
Job time : 264 secs

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Db 1139 GAATTTCCCAACCCAGAAATGTCAGAAATATCAGAGAAATGTAAGATGCTCATTCGGAAT 1198  
Qy 901 CTGCTGAAAAACAGAGCCACCCAGAGATGACCATCACCGAGTTTATGAACCAACCCCTTGG 960  
Db 1199 CTGCTGAAAAACAGAGCCACCCAGAGATGACCATCACCGAGTTTATGAACCAACCCCTTGG 1258  
Qy 961 ATCATGCAATCAACAAAGGTCCTCAAAACCCCACTGCACACACGCGGGTCTTGAAGAG 1020  
Db 1259 ATCATGCAATCAACAAAGGTCCTCAAAACCCCACTGCACACACGCGGGTCTTGAAGAG 1318  
Qy 1021 GACAAGAGCGGTGGGAGGATGTCAGAG 1050  
Db 1319 GACAAGAGCGGTGGGAGGATGTCAGAGGG 1348

## RESULT 3

US-10-505-928-626  
; Sequence 626, Application US/10505928  
; Publication No. US20060088532A1  
; GENERAL INFORMATION:  
; APPLICANT: Ludwig Institute for Cancer Research et al.  
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES  
; FILE REFERENCE: 28967/39178  
; CURRENT APPLICATION NUMBER: US/10/505,928  
; PRIOR FILING DATE: 2004-08-27  
; PRIOR APPLICATION NUMBER: US 60/363,019  
; PRIOR FILING DATE: 2002-03-07  
; NUMBER OF SEQ ID NOS: 866  
; SOFTWARE: PatentIn 3.2  
; SEQ ID NO 626  
; LENGTH: 2509  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-505-928-626

Query Match 46.7%; Score 555.8; DB 6; Length 2509;  
Best Local Similarity 72.4%; Pred. No. 2.4e-105;  
Matches 735; Conservative 0; Mismatches 277; Indels 3; Gaps 1;  
Qy 140 GCCTGCAGATCAAGAAAGCCCATCATCATGATCAAGTCAAGTCAACAGGCTCAGGCTCTGG 199  
Db 210 GCGCGGAGCCCAAGAGTACGAGTACCGAGTACCGAGTGTGTCCAAAGCAGGTGCTGG 269  
Qy 200 GGTCTGGGCATCAACGGCAAAAGTTTTCAGATCTTCAACAGAGGACCCAGGAGAAATTCG 259  
Db 270 GCTGGGTGTGAACGGCAAAAGTGTGAGTGTCTTCATCCGCGCACTGGACAGAGTGTG 329  
Qy 260 CCTCAAAATGCTTCAGGACTGCCCCAAGGCCCGCAGGAGGTGGAGCTGCACCTGGCGGG 319  
Db 330 CCTGAAGCTCTGTATGACAGCCCCCAAGGCCCGCAGGAGGTAGACCATCACTGGCAGG 389  
Qy 320 CCTCCAGTCCCGCACATGTCAGGATCTGTGATGTGTACGAGATCTGTACGAGGGA 379  
Db 390 CTTCCTGGCGGCCCAATATTTCTGTCATCTCGATGTTGTATGAGAACATCAACCATGGCA 449  
Qy 380 GGAAGTGCCTGCTGATTGTTCATGGAATGTTTGGACGGTGGAGAACTCTTTAGCCGAATCC 439  
Db 450 AGCGTGTCTCTCATCATCATGGAATGCAATGGAAGTGGTGTGAGTTGTCAGCAGGATTC 509  
Qy 440 AGGATCGAGGAGACCGGCAATTCACAGAAAGAGAGCATCCGAAATCATGAAGAGCATCG 499  
Db 510 AGGAGCGTGGCGACCGAGCTTTCATCGAGAGAGCTGCAGAGATAATCGCGGATATTG 569  
Qy 500 GTAGGCCATCCAGTATCTGCTCATCATCAACATTGCGCATCGGATGTCAAGCCTGAGA 559  
Db 570 GCACTGCGCATCCAGTTTCTGCAAGCCATCAACTTGCACCCAGAGATGTCAAGCCTGAAA 629  
Qy 560 ATCTCTTATACACTCTCAAAAGGCCCAAGCCCATCTTGAACACTCACTGACTTTTGGCTTTG 619  
Db 630 ACTTACTTACATCATTAAGGAGAAAGACGAGTGTCTTAAGCTCAACGATTTTGGCTTTG 689  
Qy 620 CCAAGGAAACCAACGACCAACTCTTTTGACCACTCTTTGTTATACACCGTACTATGTGG 679

Db 690 CTAAGGAGACCAAC--CCAAAATGCCCTGCAGACACCCCTCTATACTCCCTATTATGTGG 746  
Qy 680 CTCAGAAAGTCTGGGTCCAGAGAAAGTATGACAAAGTCTCTGTGACATGTGTCTCCCTGGGTG 739  
Db 747 CCCCTGAGGTCTGGGTCCAGAGAAAGTATGACAAAGTATGACATGTGTGTCTCCCTGGGTG 806  
Qy 740 TCATCATGTATCATCTCTGCTGTGGGTATCCCCCTTCTACTCCAAACACGCGCTTCCCA 799  
Db 807 TCATCATGTATCATCTCTTGTGGCTTCCACCCCTTCTACTCCAAACACGCGCCAGGCCA 866  
Qy 800 TCTCTCCGGCATGAAGACTTCGCATCCGAATGGGCCAGTATGAATTTTCCCAACCCAGAA 859  
Db 867 TCTCCCGGGGATGAAGAGGAGGATTCCGCTGGGCCAGTACGGCTTCCCCCAATCTCTGAGT 926  
Qy 860 GGTCAAGAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAATCTGCTGAAAAACAGAGCCCA 919  
Db 927 GGTCAAGAGTCTCTGAGGATGCCAAGCAGCTGATCCGCTCTCTGTTGAAGACAGACCCCA 986  
Qy 920 CCAGAGAAATGACCATCACCGAGTTCATGAACCAACCCCTTGATCAACCAATTCGATGGTAG 979  
Db 987 CAGAGAGGCTGACCATCACTCAGTTTCATGAACCAACCCCTTGATCAACCAATTCGATGGTAG 1046  
Qy 980 TCCTCTAAACCCCACTGCACACAGCGCGGTCTCTGAAGGAGGACAAAGAGCGGTGGGAGG 1039  
Db 1047 TGCACAGACCCCACTCCACACGCGCGAGTGTGCGAGGAGGACAAAGACCACTGGGACG 1106  
Qy 1040 ATGTCAAGGAGGATGACCAAGTGCCTTGGCCCAATTCGCGGTGTGACTAGCAGGATCA 1099  
Db 1107 AAGTCAAGGAGGATGACCAAGTGCCTTGGCCCACTATGCGGGTAGACTAGCAGCAGTGA 1166  
Qy 1100 AGATAAAAGATTGAAGATGTCATCAACCCCTCTGCTGCTGAAGAGCGCGAAGAA 1154  
Db 1167 AGATCAAGGACCTGAAGACCTTAACCAACCGGCTCTCAACAGAGGAGAGAAAA 1221

## RESULT 4

US-10-488-619-2938  
; Sequence 2938, Application US/10488619  
; Publication No. US20060099578A1  
; GENERAL INFORMATION:  
; APPLICANT: Greenlee, Winner and Sullivan, P.C.  
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations  
; FILE REFERENCE: 98-01 WO  
; CURRENT APPLICATION NUMBER: US/10/488,619  
; CURRENT FILING DATE: 2004-03-01  
; NUMBER OF SEQ ID NOS: 3040  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2938  
; LENGTH: 574  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-488-619-2938

Query Match 34.1%; Score 405.6; DB 6; Length 574;  
Best Local Similarity 91.7%; Pred. No. 9.2e-75;  
Matches 429; Conservative 0; Mismatches 39; Indels 0; Gaps 0;  
Qy 724 ATGTGTCTCTGGTGTCTCATGTATCATCTCTGCTGTGGGTATCCCCCTTCTACTCC 783  
Db 1 ATGTGTCTCTGGTGTCTCATGTATATTTTGTGTGGGTATCCCCCTTCTACTCC 60  
Qy 784 AACACGCGCTTGCATCTCTCGGCGCATGAAGACTCGCATCCGAATGGCCAGTATGAA 843  
Db 61 AATCAGCGCTTGCATCTCTCGGCGCATGAAGACTCGTATTCGAATGGCCAGTATGAA 120  
Qy 844 TTTCCCAACCCAGAAATGGTCAGAAATATCAGAGAAAGTGAAGATGCTCAATTCGGAATCTG 903  
Db 121 TTTCTTAAACCCGATTGGTCAGAAATATCAGAAAGTGAAGATGCTTATCCGAATCTG 180  
Qy 904 CTGAAACAGAGCCCAACCCAGAGAAATGACCATCACCGAGTTTATGAACCAACCTTGGATC 963

Db 181 CTAATAACAGAGCCACCCAGAGAAATGACCATCACAGAAATTCATGAACACCCCTGGATC 240  
Qy 964 ATGCAATCAACAAAGGTCCCTCAAAACCCCACTGACACACCCAGCGGTCTCTGAAGGAGGAC 1023  
Db 241 ATGCAATCTACGAAGTCCCTCAGACTCCACTGACACACCCAGCGGTCTCTGAAGGAGGAC 300  
Qy 1024 AAGAGCGGTGGAGGATGTCAAGAGGAGATGACACAGTGCCTTTGGCCACAATGCGCGTT 1083  
Db 301 AAGGAACGATGGGAGGATGTCAAGAGGAGATGACCAAGTGCCTTTGGCCACGATGCGGT 360  
Qy 1084 GACTACGAGCAGATCAAGATAAAGATTAAGATGATCAACACCTCTGCTGCTGAAG 1143  
Db 361 GACTATGAGCAGATCAAGATAAAGATTAAGAGATAGAGACGATCCAAACCTCTGCTTCTCAAG 420  
Qy 1144 AGCGGAAGAAGCTCGGGCCCTGGAGGCTGCGGCTCTGGCCCACTGA 1191  
Db 421 AGCGGAAGAAGCTCGTGTGGAGGATGCGGCTCTCGCCCACTGA 468  
RESULT 5  
US-11-217-529-2931  
; Sequence 2931, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; PRIOR FILING DATE: 2005-09-02  
; PRIOR FILING DATE: 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 2931  
; LENGTH: 1329  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-2931

Query Match 7.8%; Score 93; DB 7; Length 1329;  
Best Local Similarity 51.9%; Pred. No. 9.8e-11;  
Matches 263; Conservative 0; Mismatches 235; Indels 9; Gaps 2;  
Qy 459 ATTACAGAAGAGAACGATCCGAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCT 518  
Db 396 ATTCACGTAGGTGATGCGGTGAGAAATCCTGTTGAGATTTTAAGCGCTGTCAATACAT 455  
Qy 519 GCATTCAATCAACATGCCCCATCGGGATGTCAAGCCTGAGAATCTCTTATACACCTCCAA 578  
Db 456 GCATCCAGNATATTGTTATAGGGATTTAAACCCAGAAAATTTGCTGTATATAGATAT 515  
Qy 579 AAGGCCAACGCCATCTCTGAACTCACTGACTTTGGCTTTGGCCAGGAACACCAAGCCCA 638  
Db 516 AAGCGATGAATCTCCATTGGTGATCGCTGATTTTGGTATTGGCCAAAGAGTTTAAAGACGA 575  
Qy 639 CAACCTTTTGAC---CACTCTTGTATATACACCGTACTATGTGCTCCAGAAGTGTGGG 695  
Db 576 TGAGAGGCTATTACAAAGCAGCAGGTTCGTTGGGTTATGTGGCCCAAGATGCTTAC 635  
Qy 696 TCCAGAGAAGTATGACAAGTCTCTGACATGTGCTCCCTGGGTGCTCATGTATCATCCT 755  
Db 636 CCAAGATGGTCATGTAACCTCTGTGATATTGCTCGATTTGCTGTATCATCACATACGTT 695  
Qy 756 GCTGTGGGTATCCCGCTTCTACTCAACACCGCGCTTGCATCTCTCGGSCATGAA 815  
Db 696 GCTGTGGGTATTTCTGCATTTCAAAGCTGAAAGAGTCATGGATTTCTTTCAGC-----A 749  
Qy 816 GACTCGCATCGAATGGGCCAGTATGAATTTCCCAACCCAGAATGGTCAGAAATATCAGA 875

Db 750 GTGTACAAACCGGAAGATATCCAGTGACATTTTCATCGGCCTTATTTGGATTCAGTATCTGA 809  
Qy 876 GGAAGTGAAGATGCTCTATTTCGGAATCTGCTGAAACACAGAGCCCAACAGAGAATGACCAT 935  
Db 810 TAAAGCTAAGCGATTCATTTTGAAGCTCTTGATTTAGATCCCAACAAAGAGGCCAACCGC 869  
Qy 936 CACCGAGTTTATGAACACCCCTTTGGAT 962  
Db 870 TGCAAGAACTGTTGGAAGACCCATGGAT 896  
RESULT 6  
US-10-505-928-350  
; Sequence 350, Application US/10505928  
; Publication No. US20060088532A1  
; GENERAL INFORMATION:  
; APPLICANT: Ludwig Institute for Cancer Research et al.  
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES  
; FILE REFERENCE: 28967/39178  
; CURRENT APPLICATION NUMBER: US/10/505,928  
; PRIOR FILING DATE: 2004-08-27  
; PRIOR FILING DATE: 2002-03-07  
; NUMBER OF SEQ ID NOS: 866  
; SOFTWARE: PatentIn 3.2  
; SEQ ID NO 350  
; LENGTH: 3982  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-505-928-350  
Query Match 7.6%; Score 90.8; DB 6; Length 3982;  
Best Local Similarity 49.3%; Pred. No. 3.6e-10;  
Matches 453; Conservative 0; Mismatches 432; Indels 33; Gaps 7;  
Qy 87 GCAGCCGCGCGCGCCCGCAGCAGTTTCCCGCAGTTTCCACGTCAAGTCCGCGCTGCA 146  
Db 1382 GGAGCCCTTACAGCAAGATCTGCACAAAGTCCCAAGTTCACCAATCTGCAGCAGTTACA 1441  
Qy 147 GATCAAGAGAAACGCCCATCATCATGATGACTACAAGGTCAACAGGTCAACAGCCAGTCTCTGGGGTGGG 206  
Db 1442 CGGGAACAACATCCACTTTCACCGATGGTACGAG---ATCAAGGAGGACATCGGGTGGG 1498  
Qy 207 CATCAAGCGCAAGATTTTGCAGATCTTCAACAGAGACCCAGAGAGAAATTCGCCCTCAA 266  
Db 1499 CTCCTACTCAGTGTCAAGCGATGTGTGCATAAAGCCACAGACACCGAGTATGCGGTGAA 1558  
Qy 267 AATGCTTCAGGACTGCCCCAAGGCCCGCAGG---GAGGTGGAGCTGCACCTGGGGGCTC 323  
Db 1559 GATCATTTGATAAGAGCAGAGAGACCCCTCGGAAGAGATTGAGATCTCTCTGCGGTACGG 1618  
Qy 324 CCAGTGCCTGCACATCGTAGCGGATCGTGGATGTGTACGAAATCTGTACGAGGAGGAA 383  
Db 1619 CCAGCACCCGAAACATCATCACCTCAAGGATGTCTATGATGAT-----GGCAA 1666  
Qy 384 GTCCCTGCTGATGTGTATGGAATGTTTGGACGCTGGAGAACTCTTTAGCCGAATCCAGGA 443  
Db 1667 GTTGTGTACCTCGTAATGGAGCTGATGCGTGTGGGAGCTCTTGGACCGCATCTCCCG 1726  
Qy 444 TCAGAGAGACAGGCGATTCACAGAAAGAAAGCATCCGAATCATGAAGAGCATCGGTGA 503  
Db 1727 GCAGAGATAC-----TTCTCGGAGCGGAAGCAGTGCAGCTCTGTGCACCATCACAA 1780  
Qy 504 GGCCATCCAGTATCTGATTCATCAACATTTGCCCATCGGGATGTCAAGCCTGAGATCT 563  
Db 1781 GACCATGGACTACTCTCATTTCCAGGGGGTGTTCATCGAGACCTGAAGCCGAGTAAACAT 1840  
Qy 564 CTTATACACCTCCAAAGGCCCAACGCCAT---CCTGAAACTCACTCACTTTGGCTTTGC 620  
Db 1841 CTTGTACAGGGATGAGTTCGGGGAGCCAGAAATCCATCCGAGTCTGCGACTTTGGCTTTGC 1900  
Qy 621 CAAGGAAACCCAGGCCACAACTCTTTGACC---ACTCTTGTATTATACACCGTACTATGT 677



Db 1901 CAAGCAGCTGCGCGGGGAACGGCTGCTCATGACACCTGCTACAGCGGCAATTTGCT 1960  
Qy 678 GGCTCCAGAGTGTGGTCCAGAGAATGATGACAGTCCCTGTGACATGTGCTCCCTGGG 737  
Db 1961 GGCCCGGAGTCTGGAAGCGTCAAGCGTATGATGCGCGCGTGTGACATCTGGAGTTTGGG 2020  
Qy 738 TGTCAATGATGATGATGCTGCTGTGTTGGTATCCCGCTTCTACTCCAAACACGCGCTTGC 797  
Db 2021 GATCTGTTGATACCATGCTGGCAGGATTTACCCCTTTTGCATATGGGCGAGAC---GA 2077  
Qy 798 CATCTCTCCGGGATGAAGATCGCATCCGAATGGGCGAGTATGAAATTTCCCAACCCAGA 857  
Db 2078 TACCCCTGAGGAGATCTGGCGCGATCGGCAATGGGGAAGTATGCGCTTTCTGGGGGAAA 2137  
Qy 858 ATGCTCAGAGTATCAGGAGGATGAAGATGCTCATTCGGATCTGCTGGAACACAGAGCC 917  
Db 2138 CTGGGATCGGATATCTGACGCGATGAAGATGCTGCTCAAGATGCTTCCACGTGGGACCC 2197  
Qy 918 CACCCAGAGATGACCATCACCGAGTTTATGAACACCCCTTGGATCATGCAATCAACAAA 977  
Db 2198 TCATCAGCGCTGAGCGGATGCAAGTCTCAACACCCGTTGGTGTCAACAGAGATG 2257  
Qy 978 GGTCCCTCAACCCACT 995  
Db 2258 CCTGTCCCAACACGCT 2275

## RESULT 7

US-11-217-529-78535  
; Sequence 78535, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHIISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; PRIOR FILING DATE: 2005-09-02  
; PRIOR FILING DATE: 2005-09-02  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: Patent in version 3.3  
; SEQ ID NO 78535  
; LENGTH: 1344  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-78535

Query Match 7.4%; Score 88.2; DB 7; Length 1344;  
Best Local Similarity 49.9%; Pred. No. 9.5e-10;  
Matches 312; Conservative 0; Mismatches 298; Indels 15; Gaps 3;  
Qy 343 CGGATCGTGATGTGACGAGATCTGTACGAGGAGGAGTCCCTGCTGATTGTCATG 402  
Db 316 CCGAATCTGTGATTCAGAGGATGTTTGAATCGAAGGATTAAGTTCTATATGTCAT 375  
Qy 403 GAATGTTTGGACGGTGAGAACTCTTTAGCCGAATCCAGGATCGAGGACCCAGGATTC 462  
Db 376 CAGCTGCAACAGAGGTGATTAATTTGATAGATTTCTGTAGAGG-----GAAGTTC 429  
Qy 463 ACAGAAAGAGAGCATCCGAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCAT 522  
Db 430 ACAGAGTGTGATGCTGTGAATCATAGTTTGAATCATAGTTCTTGGTGGGAGTATATGAT 489  
Qy 523 TCAATCAACATGCCCCATCGGATGTCAAGCTTGAGATCTTTATACACCTCCAAAGG 582  
Db 490 TCAAGAAATGTTGTTTATAGATTTGAACACCTGAGAAACGTTTGTATGTTGATTAAGTCA 549

Qy 583 CCACAGCCATCTGAAACTCACTGACTTTGGCTTTGCCAAGGAAACCCACAGCCCAAC 642  
Db 550 GAAATTTGGCTCTGGTAAATTTGGGACTTCGGTATAGCTAAACAATTTGAAGGGGGAGAG 609  
Qy 643 TCTTTGA---CCACTCTCTGTTATACACCGTACTATGTGGCTCCAGAAGTGTGGGTCCA 699  
Db 610 GATTTGATATACAAAGCAGCGGATCGTTGGGCTATGTGGCACCAGAAAGTCTCCACAAA 669  
Qy 700 GAGAGTATCAGAGTCTGTGACATGTGCTCCCTGGTGTCTCATGTATGATCATCTCTG 759  
Db 670 GATGGACATGGTAAAGCCTTGTGATATATGTGCTCATTTGGTGTGATCATATCTTTACTG 729  
Qy 760 TGTGGGTATCCCGCTTCTACTCCAAACAGCGCTTGCCTCTCTCCGGGCGATGAAGACT 819  
Db 730 TCGGTTATTTCTCTTTTATTTCGGAAGCGTTGAAGGATTCATGGAGGATGTACAGCT 789  
Qy 820 CGCATCCGAATGGCCAGTATGAATTTCCAAACCCAGAAATGGTTCAGAGTATCAGAGAA 879  
Db 790 TCGAGATA-----CCCGGTAACCTTCCATATGCCATATTTGGGATACATATCTATTGAT 843  
Qy 880 GTGAGATGCTCATTCGGATCTGCTGAAACAGAGCCACCAGAGAAATGACCATCAC 939  
Db 844 GCCAAGGTTTTCATCTTGAAGGATTTGAGATTTGAATCCAGTGCACAGACCACTGTACG 903  
Qy 940 GAGTTTATGAACCAACCCCTTGGATCA 964  
Db 904 GAATTCGTGACGATCCATGGATTA 928

## RESULT 8

US-11-217-529-76461  
; Sequence 76461, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHIISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; PRIOR FILING DATE: 2005-09-02  
; PRIOR FILING DATE: 2005-09-02  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: Patent in version 3.3  
; SEQ ID NO 76461  
; LENGTH: 1341  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-76461

Query Match 7.2%; Score 85.4; DB 7; Length 1341;  
Best Local Similarity 50.9%; Pred. No. 3.5e-09;  
Matches 259; Conservative 0; Mismatches 241; Indels 9; Gaps 2;  
Qy 460 TTCAAGAAAGAGAGCATCCGAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTG 519  
Db 397 TTCCTGAGGAGATGCGATGAGAAATTTTGGTTGAAATATTTGAGCGCAGTCAAAATATG 456  
Qy 520 CATTCATCAACATCCCATCGGATGTCAAGCTTGAGAACTCTTTATACACCTCCAAA 579  
Db 457 CATTCCTCAGAAATTTGTTTATAGGACTTTGAACCCGGAATTTTATGATATAGATAAA 516  
Qy 580 AGCCCAACGCCCATCTCTGAACTCACTGACTTTGGCTTTGCCAAGGAAACCCACAGCCAC 639  
Db 517 AGTGAGAAATCTCCACTGATAGTTGCTGATTTGGTATCGCAAGAGATTTGAAGATGAT 576  
Qy 640 AACTCTTTGACC---ACTCCTTTGTTATACCGCTACTATGTGGCTCCAGAGTGTGGGT 696  
Db 577 GAGGAACTCTCTATTAAGCGCGCAGCTCACTGGGTACGTGGCTCCAGAGGTACTTACT 636

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QY 697 CCAGAGAAGTATGACAAAGTCTCTGTGACATGTGTCCTGGTGTGTCATCATGTATCATCTG 756
Db 637 CAGGACGGTCATGTGTAACCTTGGACATTTGGTCGATAGGTGTCTATTACGTATATCTTG 696
QY 757 CTGTGTGGGTATCCCCCTTCTACTCCAACACCGGCTTGGCCATCTCTCCGGGCATGAAG 816
Db 697 CTTTGGCGGTTATTTCGGCGTTTAGAGCCGAAGGGTTCAAGATTCTTCTTGACGAATGCACA 756
QY 817 ACTCGCATCCGAATGGGCCAGTATGAATTTCCCAACCCAGAATGGTCAGAAGTATCAGAG 876
Db 757 ACT-----GGTAGTATCAGTGAAGTTTCATAGGCCCTTATGGGATTCGGTTTCCAAT 810
QY 877 GAAGTGAAGATGTCATTCGGAATCTCTGTAACACAGAGCCCAACCCAGAGAATGACCATC 936
Db 811 AAGCAAAACAATTCATCTTGAAGCTCTTAATTTGGATCCTTCAAAGAGACCGACCAACC 870
QY 937 ACCGAGTTTATGAACCAACCCTTGGATCAT 965
Db 871 GCAGAACTCTTGGGAAGATCCATGGATTAT 899

RESULT 9
US-10-449-902-22824
; Sequence 22824, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22824
; LENGTH: 2390
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK072981
; DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-22824

Query Match 7.0%; Score 83; DB 6; Length 2390;
Best Local Similarity 49.2%; Pred. No. 1.3e-08;
Matches 320; Conservative 0; Mismatches 310; Indels 21; Gaps 3;

QY 346 ATCTGTGATGTACGAGAACTCTTAGCGGAGGAGTGCCTGCTGATGTGTCATCGAA 405
Db 687 AACGTGTGTGGCTCCCGGAGCGGTTCGAGAGCCCGCGCTCCACCTCGTATGGAG 746
QY 406 TGTGTGACGGTGAGAACTCTTAGCGGAATCCAGGATCGAGGAGACCGGCAATTACCA 465
Db 747 GTCTGCGAGGCGGCGAGCTCTTCGACCGCATCTGCGCCGCGGCCAC-----TACACC 800
QY 466 GAAAGAGAGCATCCGAAATCATGAAGCATCGGTGAGGCCATCCAGTATCTGCATCA 525
Db 801 GAGCGCGCGCGCGCGCGTCAATCGCACCATCATGACGCTCGTCCAGCACTGTCAAG 860
QY 526 ATCAACATTCGCCATCGGATGTCAAGCTCAGAACTCTTTATACCTCCCAAGGCC 585
Db 861 AACGGCTCATGTCATCGGACCTCAAACTGAGAACTTTCTGTATGCCAATGTCATCTGAG 920
QY 586 AACGCCATCTGAAACTCACTGACTTTGGCTTTGGCAAGGAAACCAACAGCAACTCT 645
Db 921 AACTCCCTCTCAAGGTATCGACTTCGGCTCTCAGTGTCTTCAAACCTGGTGCAAGA 980
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QY 646 TTGACCACTCCTTGTATTATACCGTACTATGTGGCTCCAGAAAGTGTGGTCCAGAGAAG 705
Db 981 TTCAATGAGATTGTTGGATCTCCCTACTACTAGCCACAGAAAGTCTCTGAAGAGA---AAC 1037
QY 706 TATGCAAGTCCCTGTGACATGTGGTCCCTGGGTGTCATCATGTGACATCTCTGTGTGGG 765
Db 1038 TATGGCAAGAATAAGACATATGGAGTGCAGGAGTCTACTGTGACATCTTGTCTATGTGGT 1097
QY 766 TATCCCCCTTCTACTCCAACCAACCGGCTTGGCATCTCTCCGGGCATGAAGATCCGCATC 825
Db 1098 GTTCTCTCTTCTGGGCGGAGACCGGACGAAGGGATCGCACAGGCCATCATCCG----- 1150
QY 826 CGAATGGCGGCAGTATGAATTTCCCAACCCAGCAATGGTCAAGATATCAGAGGAAGTGAAG 885
Db 1151 -----GTCACATATCGACTTCCAAGAGAGAGCCCTTGGCCAAAGGTGTGAGATAATGCCAAG 1205
QY 886 ATGCTCATTCGGAATCTGCTGAAAAACAGAGAGCCCAACCCAGAGAATGACCATCACCGAGTTT 945
Db 1206 GATCTTGTAAAGAGGATGCTTGTATCCAAACCATATATCTCGTTGACGGCTCAACAGTTT 1265
QY 946 ATGAACCAACCTTGGATCATGCAATCAACAAAGGTCTCCTCAAAACCCCACTG 996
Db 1266 CTAGAGCATCTTGGATACAGAATGCAAGTGCAGCTCCCAACATTCCTCTG 1316

RESULT 10
US-11-293-697-891
; Sequence 891, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTION
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 891
; LENGTH: 4098
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-891

Query Match 6.8%; Score 81.4; DB 7; Length 4098;
Best Local Similarity 49.4%; Pred. No. 3e-08;
Matches 454; Conservative 0; Mismatches 431; Indels 34; Gaps 8;

QY 87 GCAGCGCGCGCGCGCGCGCGCGCAGCAGTTCGCCGAGTTCACGTCAGTCAAGTCCGCGCTGCA 146
Db 1520 GGAGCGCTCACAGCAAGATCTGCACAAAGTCCCGAGTTCACCCCAATCTGTGACGAGTATCA 1579
QY 147 GATCAAGAAGAACGCCATCATCGATGACTACAAGGTCAACAGGCACCCAGGCTCTCTGGGGCTGG 206
Db 1580 CGGGAACAACATCACTTCAACCGATGGCTACGAG---ATCAAGGAGGACATCGGGGTGG 1636
QY 207 CATCAACGGCAAAAGTTTTCGAGATCTTCAACAGAGAGACCCAGGAGAAATTCGCCCTCAA 266
Db 1637 CTCTACTAGTGTGAAGCGATGTGTGATATAAGCCACACAGACACCGAGTATGCGGTGAA 1696
QY 267 AATGCTTCAGGACTGCCCCAAGCGCCGAGG---GAGTGCAGCTGCACATGGCGGGCTC 323
Db 1697 GATCATTTGATAGAGCAAGAGAGACCCCTCGGAAGAGATTGAGATCTCTCTGCGGTACGG 1756
QY 324 CCAGTGCCTCCACATCGTACGGATCTGTGATGTGTACAGAACTCTGTACGAGGAGGAA 383
Db 1757 CCAGCACCCGAACATCATCAACCTCAAGGATGCTATGATGAT-----GGCAA 1804
QY 384 GTGCTCTCTGATGTGTAAGAAATGTTTGGAGCGGTGGAGAACTCTTTAGCCGAATCCAGGA 443
Db 1805 GTTTGTACCTGGTATATGAGGCTGATGCGTGTGGGGAGCTCTCTGACCGCATCTCCCG 1864
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444 TCAGAGAGACGAGCAATTCACAGAAAGAGAGCAATCCGAATCATGAAGCATCGGTGA 503  
1865 GCAGAGATAC-----TTCCTGGAGCGGAAGCAGTGCCTCTGTGCACCATCACAA 1918  
504 GGCATCCAGTATCTGCATTC-A-ATCAATATGTCCTGAGTGTCAAGCCTGAGAAATC 562  
1919 GACCATGAGTATCTGCATTCATCCAGGGGGTGTTCATCGAGACCTGAAGCCGAGTAACA 1978  
563 TCTTATACATCTCAAAAGGCCCAACGCCAT--CCTGAAACTCACTGACTTTGGCTTTG 619  
1979 TCCTGTACAGGATGAGTCTGGGAGGCCAGAAATCATCCGAGTCTCGGACTTCGGCTTTG 2038  
620 CCAAGGAAACACACAGCCCAACTCTTTTGACC---ACTCCTTGTATATACCCGCTACTATG 676  
2039 CCAAGCAGCTGCGCGGGGAAACGGCTGCTCATGACACCTCTGACACGGCCAAATTCG 2098  
677 TGGCTCAGAGAGTCTGGTTCAGAGAAATGATGACAAAGTCTGTGAGATGTGTCCTGG 736  
2099 TGGCCCGGAGGTCTGAAGCGTCAAGGCTATGATGCGGGTGTGACATCTGGAATTTGG 2158  
737 GTGTATCATGTATCATCTCTGTGTGTGTATCCCTTCTACTCCAAACACGGCCTTG 796  
2159 GATCTCTGTGTACCATCTGTCAGGATTTACCCCTTTTGCAATGGGCGAGAC---G 2215  
797 CCATCTCTCCGGGCGATGAAGACTCGCATCCGAATGGGCCAGTATGAATTTCCCAACCCAG 856  
2216 ATACCCCTGAGGAGATTTGCGCGGATCGGAGTGGAGTATGCCCTTTCTGGGGAA 2275  
857 AATGGTCAGAGTATCAGAGAAAGTGAAGTGTCTATTCGGAATCTGCTGAAACAGAGC 916  
2276 ACTGGGACTCGATCTGACGCGAGCTAAAGACGTCGTGTCGAAGATGCTCAACGTCGACC 2335  
917 CCACCCAGAGATGACCATCACCGAGTTATGACACACCTTGGATCATGATCAATCAACA 976  
2336 CTATCAGCGCTGACGGCGATGCAAGTGTCTCAAAACACCCGCTGGTCAACAGAGAT 2395  
977 AGGTCCCTCAAAACCCACT 995  
2396 ACCTGTCCCCAACCACT 2414  
RESULT 11  
US-11-217-529-3295  
; Sequence 3295, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; PRIOR FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 3295  
; LENGTH: 1365  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-3295  
Query Match 6.8%; Score 81.2; DB 7; Length 1365;  
Best Local Similarity 50.4%; Pred. No. 2.6e-08;  
Matches 256; Conservative 0; Mismatches 243; Indels 9; Gaps 2;  
460 TTCACGAAAGAGAGCATCCGAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTG 519

427 TTTACAGAAATAGATGCTGTTGAGATTATAGTCACAGATCCTTGGTGTGTAGATCATC 486  
520 CATTCATCAACATTCGCCATCGGATGTCAAGCCTGAGAAATCTCTTATACACCTCCAAA 579  
487 CATTTAAAAATGTGTTTCATAGAGACTTGAACCTGAGAAATGTTTGTACGTTGACAAA 546  
580 AGCCCAACGCCATCTCTGAAACTCACTGACTTTGGCTTTGCCAAGGAAACACCCAGCCAC 639  
547 TCAGAAATTCACCTCTGTTGATTGCGGACTTTGGTATAGCTAAACAGTTGAAAGGAAA 606  
640 AACTCTTTGACCACTCTCTGTTATACACCGT---ACTATGTGGCTCCAGAAAGTCTGGGT 696  
607 GAGATTTTAAATTTATAAGCAGCTGGATCGTTGGGTTACGTGGCGCCAGAAAGTACTTACA 666  
697 CCAGAGAAAGTATGACAACTCTGTGACATCTGCTGGTGTCCCTGGGTGTCAATCATGTACATCTG 756  
667 CAAGATGGACATGAAACCCCTGTGATATATGTTAGTGTGGCGTGATCACTTACATTTTA 726  
757 CTGTGTGGTATCCCCCTTTCTACTCCAACACCGGCTTCCCATCTCTCCGGGCATGAAG 816  
727 CTCTGTGATACCTCTCGTTTCATTGCTGAAAGTGTGAGGGTTTCATGGAAGAGTGTACG 786  
817 ACTCGCATCCGAATGGCCAGTATGAATTTCCCAACCCAGAAATGGTCAGAAAGTATCAGAG 876  
787 GCT-----TCTAGATACCCGGTAACTTTCCACATGCCATCTGGGATAATATATCTATT 840  
877 GAAGTGAAGATGCTCATTCGGAATCTGCGAAACAGAGCCACCCAGAGAAATGACCATC 936  
841 GATGCTAAGCGCTTTATCTTAAAGCTTTGATGACTGAGCCGCTGATAGTAGCCGACTGATAGCCNACCGCT 900  
937 ACCGAGTTTATGAACCAACCCCTTGGATCA 964  
901 ACAGAATTGTTAGACGATCCATGATTA 928  
RESULT 12  
US-11-293-697-781  
; Sequence 781, Application US/11293697  
; Publication No. US20060105376A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: Novel full length cDNA  
; FILE REFERENCE: H1-A0106  
; CURRENT APPLICATION NUMBER: US/11/293,697  
; CURRENT FILING DATE: 2005-12-05  
; PRIOR APPLICATION NUMBER: US/10/108,260  
; PRIOR FILING DATE: 2002-03-28  
; NUMBER OF SEQ ID NOS: 5458  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 781  
; LENGTH: 2629  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-293-697-781  
Query Match 6.8%; Score 80.8; DB 7; Length 2629;  
Best Local Similarity 52.2%; Pred. No. 3.6e-08;  
Matches 237; Conservative 0; Mismatches 202; Indels 15; Gaps 2;  
530 ACATTCGCCATCGGGATGTCAAGCCTGAGAAATCTTTATACACCTCCAAAAGGCCCAACG 589  
498 ACATCGTCCACAGGACCTGAAGCCTGAGAACTCTGCTGTGGCGAGTAAATGCAAGGGTG 557  
590 CCATCCTGAAACTCACTGACTTTGGCTTTGCCAAGGAAACCCAG---CCACAATCTTT 646  
558 CGCCGCTCAAGCTGGCTGATTTTGGCTTAGCCATCGAAGTACAGGAGAGACGACGCTT 617  
647 TGACCACTCTCTGTTATACACCCGCTACTATGTGGCTCCAGAAAGTGTGGGTCCAGAGAAGT 706  
618 GGTGTTGTTTGTGTCACCCAGGTTACTTGTCCCTGAGGTCTTTGAGGAAAGATCCCT 677  
707 ATGACAAGTCTCTGTGACATGTGTCCTGGTGTGATCATGTATCATCTCTGCTGTGGGT 766

Db 678 ATGGAACCTGTGGGATATCTGGGCTGCGGGGTGTCATCTCTGTATATATCTCTCTGGTGGGCT 737  
 QY 767 ATCCCCCTTCTACTCCAAACCACGGCCTTGCCATCTCTCGGGCATGAAGACTCGCATCC 826  
 Db 738 ATCTCTCCCTTCTGGGATGAGGATCAGACAAAGCTGTATCAGCAGATCAAGCT----- 790  
 QY 827 GAATGGGCCAGTATGAATTTCCAAACCCAGAAATGGTCAAGTATCAGAGGAAGTGAAGA 886  
 Db 791 ----GGAGCCTATGATTTCCCATCAACAGATGGGACACGGTAACTCTCTGAAGCCAAGA 845  
 QY 887 TGTCTATTGGATCTCTGAAACACAGAGCCACCCAGAGAAATGACCATCACCGAGTTTA 946  
 Db 846 ACTTGATCAACACAGATGCTACCATAAACCCAGAAAGCGCATACGGCTGACCGGCTC 905  
 QY 947 TGAACCAACCTTGGATCATGCAATCAACAAGGT 980  
 Db 906 TCAAGCACCGTGGGTCTGTCAACGATCCACGGT 939

RESULT 13  
 US-10-449-902-21986  
 ; Sequence 21986, Application US/10449902  
 ; Publication No. US20060123505A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: National Institute of Agrobiological Sciences.  
 ; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
 ; APPLICANT: The Institute of Physical and Chemical Research.  
 ; APPLICANT: Foundation for Advancement of International Science.  
 ; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF  
 ; FILE REFERENCE: MOA-A0205Y1-US  
 ; CURRENT APPLICATION NUMBER: US/10/449,902  
 ; CURRENT FILING DATE: 2003-05-29  
 ; PRIORITY APPLICATION NUMBER: JP 2002-203269  
 ; PRIOR FILING DATE: 2002-05-30  
 ; PRIOR APPLICATION NUMBER: JP 2002-383870  
 ; PRIOR FILING DATE: 2002-12-11  
 ; NUMBER OF SEQ ID NOS: 56791  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 21986  
 ; LENGTH: 2641  
 ; TYPE: DNA  
 ; ORGANISM: Oryza sativa  
 ; PUBLICATION INFORMATION:  
 ; DATABASE ACCESSION NUMBER: AK072204  
 ; DATABASE ENTRY DATE: 2001-12-06  
 US-10-449-902-21986

Db	1536	AGTTCTGAA---AAAGAAATATGGTCAAGAGGCAGATGTCGAGAGCCCTGGTGTGTAAT	1592
Qy	747	GTACATCTCTGCTGTGGGTATCCCCCTTCTACTCCAACACAGCGCCTTGCCATCTCTCC	806
Db	1593	TTACATCTTGTGTGGTGTGCGGCATTTTGGGCAGAGAACGAGCAGGTATATTGA	1652
Qy	807	GGGCATGAAGACTCGCATCCGAATGGCCAGTATGAATTTCCCAACCCAGAAATGGTCAGA	866
Db	1653	AGAGGTTTTCATCGTGGTAGAC-----TTGACTTTTCAGTCAGAAACCATGGCCCTAG	1700
Qy	867	AGTATCAGAGGAAGTGAAGATGTCATTTCGGAATCTCTGAAAAACAGAGCCACCCAGAG	926
Db	1701	CATCTCTGAAGTGGCCAAAGATCTCTGAAGAGAAATGCTTGTAGGACCCGAGAGAG	1760
Qy	927	AATGACCATCACCAGGTTTATGAACCAACCCTTGGATCATGCAATCAACAAGTCCCTCA	986
Db	1761	ATTGACAGCTCATGAAGTTTAAAGGCATCCATGGGTCAGGTTGGTGGTTGGCTCCTGA	1820
Qy	987	AACCCCACTGCA	998
Db	1821	CAAGCCCTCGA	1832
RESULT 14			
US-11-312-958-35			
; Sequence 35, Application US/11312958			
; Publication No. US20060100152A1			
; GENERAL INFORMATION:			
; APPLICANT: Millennium Pharmaceuticals, Inc.			
; APPLICANT: Rosenfeld, Julie Beth			
; APPLICANT: Silos-Santiago, Immaculada			
; TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING			
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 9949, 14230, 760, 62553,			
; TITLE OF INVENTION: 12216, 17719, 41897, 47174, 33408, 10002, 18209, 314, 636,			
; TITLE OF INVENTION: 27410, 33260, 619, 15985, 69112, 2158, 224, 615, 44373,			
; TITLE OF INVENTION: 95431, 2245, 2387, 16658, 55054, 16314, 1613, 1675, 9569 OR			
; TITLE OF INVENTION: 13424 MOLECULES			
; FILE REFERENCE: MPI02-027PIRNONMIM			
; CURRENT APPLICATION NUMBER: US/11/312,958			
; CURRENT FILING DATE: 2005-12-20			
; PRIOR APPLICATION NUMBER: US/10/369,022			
; PRIOR FILING DATE: 2003-02-19			
; PRIOR APPLICATION NUMBER: US 60/360,495			
; PRIOR FILING DATE: 2002-02-28			
; PRIOR APPLICATION NUMBER: US 60/370,121			
; PRIOR FILING DATE: 2002-04-04			
; PRIOR APPLICATION NUMBER: US 60/373,010			
; PRIOR FILING DATE: 2002-04-16			
; PRIOR APPLICATION NUMBER: US 60/373,908			
; PRIOR FILING DATE: 2002-04-19			
; PRIOR APPLICATION NUMBER: US 60/377,717			
; PRIOR FILING DATE: 2002-05-03			
; PRIOR APPLICATION NUMBER: US 60/379,949			
; PRIOR FILING DATE: 2002-05-13			
; PRIOR APPLICATION NUMBER: US 60/382,409			
; PRIOR FILING DATE: 2002-05-21			
; PRIOR APPLICATION NUMBER: US 60/385,280			
; PRIOR FILING DATE: 2002-06-03			
; PRIOR APPLICATION NUMBER: US 60/386,879			
; PRIOR FILING DATE: 2002-06-06			
; Remaining Prior Application data removed - See File Wrapper or PALM.			
; NUMBER OF SEQ ID NOS: 64			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 35			
; LENGTH: 2421			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (91)...(2058)			
US-11-312-958-35			

Best Local Similarity 47.9%; Pred. No. 5.7e-08;  
Matches 401; Conservative 0; Mismatches 412; Indels 24; Gaps 5;

QY 133 AAGTCCGGCTGCAGATCAAGAGAACGCCATCATCGATCAAGTACCAAGTCCAGCCAG 192  
Db 1132 AAGCCAGCCCATGGGCATCATTTGCCGCAATGTGAAAGCAATATGAGACTGGCCGG 1191  
QY 193 GTCTGGGGCTGGGCATCAACGGCAAAAGTTTTCAGATCTTCAACAAGAGAGCCAGGAG 252  
Db 1192 GTCAATGGGATGGAACTTTGCTGCTGAAGAGTGCAGACACCCGAGAGCCAGGAG 1251  
QY 253 AAATTCGCCCTCAAAATGCTTTCAGGATGCCCCAAGCCCGCAGGAGGTGGAGTGCAC 312  
Db 1252 GCCTATGCGATGAAGATCATTTACAAGTCCAGACTCAAGGCAAGGAGGACATGGTGGAC 1311  
QY 313 TGGCGGCTCCAGTCCCGCATCATCGTACGGATCGTGGATGTGTACGAGAT---CTG 369  
Db 1312 AGTAGATCTTGATCATCCAGAGCTCTCACCCCAACATCGTGAATTTGCATGAAGTC 1371  
QY 370 TACGAGGAGGAGTGCCTGCTGATTGTGATGAAATGTTTGGACGGTGGAGAACTCTTT 429  
Db 1372 TACGAAACAGACATGGAATCTACCTGATCTTGGAGTACGTGAGGAGGAGACCTTTT 1431  
QY 430 AGCGGAATCAGGATCAGGAGACCGGATTCACAGAAAGAGAGCATCCGAAATCATG 489  
Db 1432 GACGCCCATATAGAAAGT-----TGAAGTCCCGAGGCCGATGCTGCCCTCATGATC 1485  
QY 490 AAGAGATCGGTGAGGCCATCCAGTATCTGCATTCATCAACATTCGCCATCGGATGTC 549  
Db 1486 ATGGACTTATGAAAGCCCTCGTCCACATGCAGCAAGAGCATTTGCCACCGGACCTC 1545  
QY 550 AAGCTGAGAAATCTTTATACACTCCAAAGGCCCAA-----CGCCATCTGAAACTCACT 606  
Db 1546 AAGCCGGAACCTTTTGGTTACAGGAATGAGGACAAATCTACTACTTGAATTTGGCT 1605  
QY 607 GACTTTGGCTTTGCCAAGGAAACACAGCCCAAACTCTTTGACCACTCTCTTTATATA 666  
Db 1606 GATTTTGGACTTGCAGAGCATGTGGTGAGAC-----CTATATTTACTGTGTGGGACC 1659  
QY 667 CGGTACTATGTGCTCCAGAGTCTGGGTCCAGAGAGTATGACAAGTCTGTGACATG 726  
Db 1660 CCAACTTACTAGCTCCGAAATCTTTCTGAGAAAGTTTATGAGTGGAGTGAGCATG 1719  
QY 727 TGGTCCCTGGGTGATCATATGATATCTGCTGTGGGTATCCCGCTTCTACTCCAAC 786  
Db 1720 TGGGCTGCTGGGTGATCTCTATATCTCTGCTGTGGCTTTCCCGCATTCGACCCCT 1779  
QY 787 CAGGCTTGGCATCTCTCGGCGCATGAAGACTCGCATCCGAATCGGACAGTATGAATTT 846  
Db 1780 GAGAGGACCGAGGACGAGCTCTTTAACA-----TCATCCAGCTGGGCCACTTTGAGTTC 1833  
QY 847 CCCAACCCAGAAATGGTCAAGATPATCAGAGGAGTGAAGATGCTCATTCGGAATCTGCTG 906  
Db 1834 CTCCTCCCTTACTGGGACAAATCTCTGATGCTGCTAAAGATCTGGTGGCCGTTGCTG 1893  
QY 907 AAAACAGAGCCACCCAGAGAAATGACCATCACCGAGTTTATGAACACCCCTTGGATC 963  
Db 1894 GTGGTAGACCCCAAAAGCGCTACACAGCTCATCAGTTCTTCAGACCCCTGGATC 1950

RESULT 15  
US-11-312-958-3  
; Sequence 3, Application US/11312958  
; Publication No. US20060100152A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc.  
; APPLICANT: Rosenfeld, Julie Beth  
; APPLICANT: Silos-Santiago, Immaculada  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING  
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 9949, 14230, 760, 62553,  
; TITLE OF INVENTION: 12216, 17719, 41897, 47174, 33408, 10002, 16209, 314, 636,  
; TITLE OF INVENTION: 27410, 33260, 619, 15985, 69112, 2158, 224, 615, 44373,  
; TITLE OF INVENTION: 95431, 22245, 2387, 16658, 55054, 16314, 1675, 9569 OR

; TITLE OF INVENTION: 13424 MOLECULES  
; FILE REFERENCE: MPI02-027PIRNOMIN  
; CURRENT APPLICATION NUMBER: US/11/312,958  
; CURRENT FILING DATE: 2005-12-20  
; PRIOR APPLICATION NUMBER: US/10/369,022  
; PRIOR FILING DATE: 2003-02-19  
; PRIOR APPLICATION NUMBER: US 60/360,495  
; PRIOR FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: US 60/370,121  
; PRIOR FILING DATE: 2002-04-04  
; PRIOR APPLICATION NUMBER: US 60/373,010  
; PRIOR FILING DATE: 2002-04-16  
; PRIOR APPLICATION NUMBER: US 60/373,908  
; PRIOR FILING DATE: 2002-04-19  
; PRIOR APPLICATION NUMBER: US 60/377,717  
; PRIOR FILING DATE: 2002-05-03  
; PRIOR APPLICATION NUMBER: US 60/379,949  
; PRIOR FILING DATE: 2002-05-13  
; PRIOR APPLICATION NUMBER: US 60/382,409  
; PRIOR FILING DATE: 2002-05-21  
; PRIOR APPLICATION NUMBER: US 60/385,280  
; PRIOR FILING DATE: 2002-06-03  
; PRIOR APPLICATION NUMBER: US 60/386,879  
; PRIOR FILING DATE: 2002-06-06  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 4726  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (2)...(1828)  
US-11-312-958-3

Query Match 6.7%; Score 79.8; DB 7; Length 4726;  
Best Local Similarity 47.9%; Pred. No. 6.6e-08;  
Matches 401; Conservative 0; Mismatches 412; Indels 24; Gaps 5;

QY 133 AAGTCCGGCTGCAGATCAAGAGAACGCCATCATCGATCAAGTACCAAGTCCAGCCAG 192  
Db 902 AAGCCAGCCCATGGGCATCATTTGCCGCAATGTGAAAGCAATATGAGACTGGCCGG 961  
QY 193 GTCTGGGGCTGGGCATCAACGCCAAGTTTTCAGATCTTCAACAAGAGGACCCAGGAG 252  
Db 962 GTCAATGGGGTGGGAACCTTTGCTGTGTAAGGAGTGCAGACACCCGAGAGCCAGGAG 1021  
QY 253 AAATTCGCCCTCAAAATGCTTTCAGGACTGCCCAAGGCCCGCAGGAGGTGGAGTGCAC 312  
Db 1022 GCCTATGCGATGAAGATCATTCGAACTCCAGACTCAAGGCAAGGAGACATGGTGGAC 1081  
QY 313 TGGCGGCTCCAGTGGCCGACATCGTACGGATGTGTGAGATGTGTACAGAAAT---CTG 369  
Db 1082 AGTGAGATTTGATCATCCAGAGCCTCTCTACCCCAACATCGTGAATTTGATGAAGTC 1141  
QY 370 TACGAGGAGGAGTGGCTGCTGATTTGATGGAATGTTTCGACGGTGGAGAACTCTTT 429  
Db 1142 TACGAAACAGACATGAAATCTACTGATCTCTGGAGTACGTGAGGAGGAGACCTTTT 1201  
QY 430 AGCCGAATTCAGGATCGAGGAGACCGAGCATTCACAGAAAGAGAGCATCCGAAATCATG 489  
Db 1202 GAGCCATCATAGAAGTG-----TGAAGTTCCCGAGGCCGATGCTGCCCTCATGATC 1255  
QY 490 AAGAGCATCGGTGAGGCCATTCAGTATCTGCAATCAATCAACATTCGCCATCGGATGTC 549  
Db 1256 ATGGACTTATGCAAGCCCTCGTCCACATGCAGCAAGAGCATTTGTCCACCGGAGCCTC 1315  
QY 550 AAGCTGAGAAATCTCTTATACACTCCAAAGGCCCAA---CGCCATCTGAAACTCACT 606  
Db 1316 AAGCCGGAACCTTTTGGTTCAGGAAATGAGGACAAATCTACTACCTTGAATTTGGCT 1375  
QY 607 GACTTTGGCTTTGCCAAGGAAACCCAGCCCAAACTCTTTTGACCACTCTCTTTTATATA 666

Db	1376	GATTTTGGACTTGGCAAGCATGTGTGAGAC-----CTATATTTACTGTGTGGGACC	1429
Qy	667	CCGTACTATGTGGCTCCAGAGTGTGGGTCCAGAGAGTATGACAAAGTCTCTGTGACATG	726
Db	1430	CCAACTTACGTAGCTCCCGAATTCTTCTGAGAAAGGTTATGGACTGGAGGTGGACATG	1489
Qy	727	TGGTCCCTGGGTGTGATCATGTACATCCTGTGTGTGGGTATCCGCCCTTCTACTCCAAC	786
Db	1490	TGGGCTGTGGCGTGATCCTCTATATCTCTGTGTGGCTTTCCCCCATTCGCCAGCCCT	1549
Qy	787	CACGGCTTGGCATCTCTCCGGCATGAAGACTCGCATCCGAATGGGCCAGTATGAATTT	846
Db	1550	GAGAGGACCCAGGACGAGCTCTTTAACA-----TCATCCAGCTGGGCCACTTTGAGTTC	1603
Qy	847	CCCAACCCAGAAATGGTCAAGATATCAGAGGAAGTGAAGATGCTCATTCGGAATCTGCTG	906
Db	1604	CTCCCCCTTACTGGGACAAATATCTCTGATGCTGCTAAAGATCTGGTGAGCCGGTTGCTG	1663
Qy	907	AAAAAAGAGCCCAACCCAGAGATGACCATCACCGAGTTTATGAACACCCCTTGGATC	963
Db	1664	GTGGTAGACCCCAAAAGCGCTACACAGCTCATCAGGTTCTTCAGACCCCTGGATC	1720

Search completed: June 19, 2006, 17:14:27  
Job time : 73 secs

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2006, 15:49:29 ; Search time 848 Seconds  
(without alignments)  
9792.391 Million cell updates/sec

Title: US-10-469-221-1  
Perfect score: 1191  
Sequence: 1 tccaggccagagccgcgc.....ctggcgctctggccactga 1191

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq\_8.\*

1: Geneseqn1980s.\*  
2: Geneseqn1990s.\*  
3: Geneseqn2000s.\*  
4: Geneseqn2001as.\*  
5: Geneseqn2001bs.\*  
6: Geneseqn2002as.\*  
7: Geneseqn2002bs.\*  
8: Geneseqn2003as.\*  
9: Geneseqn2003bs.\*  
10: Geneseqn2003cs.\*  
11: Geneseqn2003ds.\*  
12: Geneseqn2004as.\*  
13: Geneseqn2004bs.\*  
14: Geneseqn2005s.\*  
15: Geneseqn2006s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1191	100.0	1191	8 AAD50036	Aad50036 Human tru
2	1191	100.0	1203	8 AAD50037	Aad50037 Human ful
3	1186.2	99.6	1203	14 ADV43403	Adv43403 Human psy
4	1186.2	99.6	1726	12 ADM36339	Adm36339 Human MK2
5	1186.2	99.6	1726	14 ADX06659	Adx06659 Cyclin-de
6	1181.4	99.2	1336	11 ADI32071	Adi32071 Human cdn
7	1181.4	99.2	1336	6 ABK84657	Abk84657 Human cdn
8	1181.4	99.2	1336	13 ADS84138	Ads84138 Human lym
9	1080.2	90.7	2802	3 AAF15803	Aaf15803 Human pro
10	1050.4	88.2	2592	13 ACN41322	Acn41322 Human dia
11	1048.4	88.0	1113	14 ADV43402	Adv43402 Human psy
12	1048.4	88.0	1128	6 ADP87584	Adp87584 Human NOV
13	1048.4	88.0	2258	12 ABL67227	Ab167227 Thyroid c
14	1048.4	88.0	2258	10 ACA56817	Acas56817 Human sig
15	1048.4	88.0	2258	12 ACA56613	Adi56613 Human pol
16	1048.4	88.0	2258	12 ADP87578	Adp87578 Human NOV
17	1048.4	88.0	2258	14 AED17914	Aed17914 Fibrotic
18	1048.4	88.0	2263	6 ABV73995	Abv73995 Human MAP

19	1048.4	88.0	2263	9 ACA62272	Acas62272 Human DNA
20	1048.4	88.0	2263	12 ADM36337	Adm36337 Human MK2
21	1048.4	88.0	2263	14 ADX06657	Adx06657 Cyclin-de
22	1048.4	88.0	2263	14 ADY86797	Ady86797 Human MAP
23	1048.4	88.0	2263	14 AEA89439	Aea89439 Human MAP
24	1048.4	88.0	3608	14 ADZ49304	Adz49304 Insulin s
25	1038.8	87.2	1130	12 ADP87582	Adp87582 Human NOV
26	1038.8	87.2	1133	12 ADP87586	Adp87586 Human NOV
27	1002.4	84.2	1026	12 ADP87588	Adp87588 Human NOV
28	982	82.5	1305	9 ACF57389	Acf57389 SUMO-MPAK
29	972	81.6	981	12 ADN61587	Adn61587 DNA encod
30	904.4	75.9	3186	8 ACC46238	Acc46238 Human dit
31	876.8	73.6	885	12 ADP87580	Adp87580 Human NOV
32	876.8	73.6	885	12 ADP87590	Adp87590 Human NOV
33	836.4	70.2	1168	14 AEE13869	Aee13869 Hamster c
34	591.4	49.7	690	12 ADP87652	Adp87652 Rat MAPKA
35	582	47.2	614	14 ACL61582	Acc61582 Human col
36	555.8	46.7	1149	14 AEE19658	Aee19658 Human MAP
37	555.8	46.7	1298	6 ABK84332	Abk84332 Human cdn
38	555.8	46.7	2481	6 ABK84214	Abk84214 Human cdn
39	555.8	46.7	2481	6 ABK13301	Abk13301 DNA encod
40	555.8	46.7	2481	10 ADD14766	Add14766 Human src
41	555.8	46.7	2481	10 ACA56490	Acas6490 Human sig
42	555.8	46.7	2481	12 ADI56286	Adi56286 Human pol
43	555.8	46.7	2481	12 ADO52389	Ado52389 Human BRC
44	555.8	46.7	2500	12 ADP21372	Adp21372 Gene MAPK
45	555.8	46.7	2500	12 ADQ87216	Adq87216 Human tum

## ALIGNMENTS

RESULT 1

AAD50036

ID AAD50036 standard; cDNA; 1191 BP.

XX

AC AAD50036;

XX

DT 24-MAR-2003 (first entry)

XX

DE Human truncated MAPKAP-2 kinase, tdnMAPKAP-2 cDNA.

XX

KW Human; mitogen-activated protein kinase activating protein kinase-2;

KW MAPKAP-2 kinase; signal transduction; cell proliferative disorder;

KW immune system disorder; inflammation; arthritis; immunomodulator;

KW cytostatic; gene therapy; enzyme; gene; ss.

XX Homo sapiens.

OS

XX

FT Key Location/Qualifiers

FT CDS 1..1191

FT /\*tag= a

FT /product= "Human tdnMAPKAP-2"

FT /note= "No start codon"

FT /partial

XX

XX WO200290524-A2.

PN

XX

XX

PD 14-NOV-2002.

XX

XX

PF 25-FEB-2002; 2002WO-US005670.

XX

PR 28-FEB-2001; 2001US-0272260P.

XX

XX (MERI ) MERCK & CO INC.

PA

XX

XX

PI Lograsso P, Hawkins J, Lisnock JM;

XX

XX WPI; 2003-111970/10.

DR P-PSDB; AAE29898.

XX

XX New isolated nucleic acid molecule encoding a human mitogen-activated

PT protein kinase activating protein kinase-2 (MAPKAP-2), useful for







XX	Sequence	1203 BP; 303 A; 365 C; 313 G; 222 T; 0 U; 0 Other;
SQ	Query Match	99.6%; Score 1186.2; DB 14; Length 1203;
	Best Local Similarity	99.7%; Pred. No. 2.1e-259;
	Matches 1188; Conservative	0; Mismatches 3; Indels 0; Gaps 0;
Qy	1	TCCAGGCGCAGAGCCCGCGGTGCGTTCCCGCCCCCGCGCGCGAGCCCGCC 60
Db	13	TCCAGGCGCAGAGCCCGCGGTGCGTTCCCGCCCCCGCGCGCGAGCCCGCC 72
Qy	61	ACCCCTCGCTGCGCAGCCCGCGCGCGCGCGCGCGCGCGCGCGAGGTCCTCG 120
Db	73	ACCCCTCGCTGCGCAGCCCGCGCGCGCGCGCGCGCGCGCGCGAGGTCCTCG 132
Qy	121	CAGTTCACGCTCAAGTCCGGCTCGCAGATCAAGAAGAACGCCATCATCGATGACTACAAG 180
Db	133	CAGTTCACGCTCAAGTCCGGCTCGCAGATCAAGAAGAACGCCATCATCGATGACTACAAG 192
Qy	181	GTACACCGCAGGTCCTGGGGCTGGGCATCAACGGCAAAAGTTTTCAGATCTTCAACAAG 240
Db	193	GTACACCGCAGGTCCTGGGGCTGGGCATCAACGGCAAAAGTTTTCAGATCTTCAACAAG 252
Qy	241	AGGACCCAGGAGAAATTCGCCCTCAAAATGCTTCAGGACTGCCCAAGGCCCGCAGGGAG 300
Db	253	AGGACCCAGGAGAAATTCGCCCTCAAAATGCTTCAGGACTGCCCAAGGCCCGCAGGGAG 312
Qy	301	GTGGAGCTGCACTGGCGGGCTCCAGTGGCCGCACATCGTACGGATCGTGGATGTGTAC 360
Db	313	GTGGAGCTGCACTGGCGGGCTCCAGTGGCCGCACATCGTACGGATCGTGGATGTGTAC 372
Qy	361	GAGAACTGTACGAGGAGGAAGTCTGCTGATGTTGTCATGAAATTTTGGACGTGGGA 420
Db	373	GAGAACTGTACGAGGAGGAAGTCTGCTGATGTTGTCATGAAATTTTGGACGTGGGA 432
Qy	421	GAATCTTTAGCGAATTCAGGATTCAGAGGACGAGCATTCAAGAAAGAGAGCATCC 480
Db	433	GAATCTTTAGCGAATTCAGGATTCAGAGGACGAGCATTCAAGAAAGAGAGCATCC 492
Qy	481	GAATCATGAAGCATCGGTAGGCCATCCAGTATCTGATTTCAATCAATTTGCCCAT 540
Db	493	GAATCATGAAGCATCGGTAGGCCATCCAGTATCTGATTTCAATCAATTTGCCCAT 552
Qy	541	CGGATGTCAAGCTGAGAACTCTTATACCTTCAAAAGGCCCAAGCCATCTCTGAAA 600
Db	553	CGGATGTCAAGCTGAGAACTCTTATACCTTCAAAAGGCCCAAGCCATCTCTGAAA 612
Qy	601	CTCACTGACTTTGGCTTTGCCAAGAAACCAAGCCACCAACTCTTTGACCACTCTCTGT 660
Db	613	CTCACTGACTTTGGCTTTGCCAAGAAACCAAGCCACCAACTCTTTGACCACTCTCTGT 672
Qy	661	TATACACCGTACTATGTGGCTCCAGAGTGCTGGGTCCAGAGAGTATGACAAGTCTGT 720
Db	673	TATACACCGTACTATGTGGCTCCAGAGTGCTGGGTCCAGAGAGTATGACAAGTCTGT 732
Qy	721	GACATGTGCTCCCTGGGTGTCATCATCTGCTGTGTTGGGTATCCCGCTTCTAC 780
Db	733	GACATGTGCTCCCTGGGTGTCATCATCTGCTGTGTTGGGTATCCCGCTTCTAC 792
Qy	781	TCCAACCAAGCCCTTGGCATCTCTCCGGGATGAAGACTCGCATCCGAATGGGCGAGTAT 840
Db	793	TCCAACCAAGCCCTTGGCATCTCTCCGGGATGAAGACTCGCATCCGAATGGGCGAGTAT 852
Qy	841	GAATTTCCCAACCCAGAAATGGTCAAGAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT 900
Db	853	GAATTTCCCAACCCAGAAATGGTCAAGAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT 912
Qy	901	CTGCTGAAACACAGAGCCACCCAGAGATGACCATCACCGAGTTTATGAACCCCTTGG 960
Db	913	CTGCTGAAACACAGAGCCACCCAGAGATGACCATCACCGAGTTTATGAACCCCTTGG 972
Qy	961	ATCATGCAATCAACAAAGGTCCCTCAAAACCCCACTGCACACCCAGCCGGTCTTGAAGGAG 1020

Db	973	ATCATGCAATCAACAAAGGTCCCTCAAAACCCCACTGCACACAGCGGGTCTCTGAAGGAG 1032
Qy	1021	GACAAGGAGCGGTGGGAGGATGTCAAGGAGGAGATGACCAAGTGCCTTTGGCCACAATGCGC 1080
Db	1033	GACAAGGAGCGGTGGGAGGATGTCAAGGAGGAGATGACCAAGTGCCTTTGGCCACAATGCGC 1092
Qy	1081	GTTGACTACGAGCAGATCAAGATAAAAAAGATTGAAGATGATCCAAACCTCTGCTGCTG 1140
Db	1093	GTTGACTACGAGCAGATCAAGATAAAAAAGATTGAAGATGATCCAAACCTCTGCTGCTG 1152
Qy	1141	AACAGCGGGAAGAAAGCTCGGGCCCTGGAGGCTCGGCTCTGGCCCACTGA 1191
Db	1153	AACAGCGGGAAGAAAGCTCGGGCCCTGGAGGCTCGGCTCTGGCCCACTGA 1203
RESULT 4		
ADM36339		
ID	ADM36339	standard; cDNA; 1726 BP.
XX	AC	ADM36339;
XX	DT	03-JUN-2004 (first entry)
XX	XX	Human MK2 variant 2 encoding cDNA SEQ ID NO:3.
DE	XX	ischaemic injury;
XX	XX	mitogen-activated protein kinase-activated protein kinase 2; MK2;
KW	KW	vasotrophic; cerebroprotective; cardiact; hypotensive;
KW	KW	antiarteriosclerotic; thrombolytic; neuroprotective; cardiovascular;
KW	KW	antianginal; antiarrhythmic; MK2 antagonist; cerebral ischaemia;
KW	KW	ischaemia; vascular occlusion; cerebral infarction; stroke;
KW	KW	cerebral vascular disease; myocardial infarction;
KW	KW	coronary artery disease; congestive heart failure; cardiac arrhythmia;
KW	KW	unstable angina; high blood pressure; claudication;
KW	KW	peripheral occlusive arterial disease; atherosclerosis;
KW	KW	thrombotic condition; thromboembolic condition; CNS disorder; human;
KW	KW	MK2 variant 2; chromosome 1q32; gene; ss.
XX	OS	Homo sapiens.
XX	XX	
XX	Key	Location/Qualifiers
FT	379.	.1581
CDS		/*tag= a
FT	/product=	"MK2 variant 2"
FT		
XX	WO2004017909-A2..	
PN		
XX	04-MAR-2004.	
XX		
XX	21-AUG-2003;	2003WO-US026337.
XX		
PR	23-AUG-2002;	2002US-0405586P.
XX		
XX	(BRIM )	BRISTOL-MYERS SQUIBB CO.
XX		
PI	Wang X,	Schieven G, Feuerstein GZ;
XX		
DR	WPI;	2004-226726/21.
DR	P-PSDB;	ADM36340.
XX		
XX	Reducing or treating ischemic injury,	comprises administering an
PT	inhibitor of mitogen-activated protein kinase-activated protein kinase 2	
PT	(MK2) activity or expression.	
XX		
PS	Disclosure;	SEQ ID NO 3; 39pp; English.
XX		
CC	The present invention describes a method for reducing ischaemic injury in	
CC	a mammal, which comprises administering a compound that reduces the	
CC	activity of mitogen-activated protein kinase-activated protein kinase 2	
CC	(MK2) or that inhibits MK2 expression. Also described: (1) identifying a	
CC	compound which inhibits MK2 expression in a cell, or which modulates MK2	
CC	activity; (2) compounds identified by the method above; and (3) treating	
CC	ischaemic injury by administering to a patient a compound above, or an	

Db	1171	TCCAACACAGCGCCTTGCATCTCTCCGGGCGATGAAGACTCGCATCCGAATGGCGCAGTAT	1230
Qy	841	GAATTTCCCAACCCAGAAATGGTCAGAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT	900
Db	1231	GAATTTCCCAACCCAGAAATGGTCAGAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT	1290
Qy	901	CTGCTGAAAAACAGAGCCCAACCCAGAGAAATGACCATCACCGAGTTTATGAACACCACTCTGG	960
Db	1291	CTGCTGAAAAACAGAGCCCAACCCAGAGAAATGACCATCACCGAGTTTATGAACACCACTCTGG	1350
Qy	961	ATCATGCAATCAACAAAGAGTCCCTCAAACCCCACTGCACACCAAGCCGGGTCCCTGAAGAG	1020
Db	1351	ATCATGCAATCAACAAAGTCCCTCAAACCCCACTGCACACCAAGCCGGGTCCCTGAAGAG	1410
Qy	1021	GACAAGAGCGGTGGGAGGATGTCAAGGAGGAGATGACCAAGTGCCTTTGGGCCACAAATGCGC	1080
Db	1411	GACAAGAGCGGTGGGAGGATGTCAAGGAGGAGATGACCAAGTGCCTTTGGGCCACAAATGCGC	1470
Qy	1081	GTTGACTACGAGCAGATCAAGATAAAAAAGATTGAAGATGCATCCAAACCTCTGCTGCTG	1140
Db	1471	GTTGACTACGAGCAGATCAAGATAAAAAAGATTGAAGATGCATCCAAACCTCTGCTGCTG	1530
Qy	1141	AAGAGCGGGAAGAAAGCTCGGGCCCTGGAGGCTGCGGCTCTGGGCCACTGA	1191
Db	1531	AAGAGCGGGAAGAAAGCTCGGGCCCTGGAGGCTGCGGCTCTGGGCCACTGA	1581

RESULT 5	
ADX06659	
ID	ADX06659 standard; DNA; 1726 BP.
XX	
AC	ADX06659;
XX	
DT	21-APR-2005 (first entry)
XX	
DE	Cyclin-dependent kinase modulation biomarker DNA SEQ ID NO 1224.
XX	
XX	cytostatic; cyclin-dependent kinase; cdk; biomarker; gene; ds.
KW	
XX	
OS	Homo sapiens.
XX	
FN	WO2005012875-A2.
XX	
PD	10-FEB-2005.
XX	
XX	
PF	29-JUL-2004; 2004WO-US024424.
XX	
PR	29-JUL-2003; 2003US-0490890P.
XX	
PA	(BRIM ) BRISTOL-MYERS SQUIBB CO.
XX	
PI	Li M, Rupnow BA, Webster KR, Jackson DG, Wong TW;
XX	
DR	WPI; 2005-163068/17.
DR	P-PSDE; ADX06660.
XX	
PT	Biomarkers useful for predicting or determining the response of a mammal
PT	to a cancer treatment comprising administration of a modulator of cyclin-
PT	dependent kinase activity.
XX	
PS	Claim 5; SEQ ID NO 1224; 141pp; English.
XX	
CC	This invention describes a novel method of predicting or determining
CC	whether a mammal will respond or is responding to an anti-cancer agent
CC	that modulates cyclin-dependent kinase (cdk) activity. The method
CC	comprises measuring the level of one or more biomarkers selected from
CC	2774 biomarkers given in the specification (nucleotide sequence SEQ ID
CC	NO:1246 (Genbank EST W28729) is especially preferred). The method of the
CC	invention is utilized in a kit for determining or predicting whether
CC	patient would be susceptible or resistant to treatment by an agent
CC	modulating cdk activity. The invention also describes a method for
CC	utilizing individualized genetic profiles for treating diseases and

CC disorders based on patient's response and molecular level, specialized  
CC microarrays comprising the biomarkers described, antibodies directed  
CC against the biomarkers and a cell culture model to identify biomarkers.  
CC The cdk modulator is preferably N-5-[(5-(1,1-dimethylethyl)-2-  
CC oxazolyl)methylthio]-2-thiazolyl-4-piperidine carboxamide, 0.5-L-  
CC tartaric acid salt. Note: The sequence data for this patent did not form  
CC part of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences. This  
CC sequence encodes a biomarker used in the method of the invention.  
XX  
SQ Sequence 1726 BP; 411 A; 543 C; 481 G; 291 T; 0 U; 0 Other;  
  
Query Match 99.68; Score 1186.2; DB 14; Length 1726;  
Best Local Similarity 99.78; Pred. No. 2.3e-259; Indels 0; Gaps 0;  
Matches 1188; Conservative 0; Mismatches 3;  
  
Qy 1 TCCAGGCGCAGAGCCCGCGGTGCGTTCCTCCGCGCCCGCGCGCGCGCGCGCC 60  
Db 391 TCCAGGCGCAGAGCCCGCGGTGCGTTCCTCCGCGCCCGCGCGCGCGCGCC 450  
  
Qy 61 ACCCTGCTCCGCGACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120  
Db 451 ACCCTGCTCCGCGACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 510  
  
Qy 121 CAGTTCACGTCAGTCCGCGCTGCAGATCAAGAAGAACGCGCATCATCGATGACTACAAG 180  
Db 511 CAGTTCACGTCAGTCCGCGCTGCAGATCAAGAAGAACGCGCATCATCGATGACTACAAG 570  
  
Qy 181 GTACACGCGAGGTCCTGGGGCTGGGCATCAACGGCAAAAGTTTGTGAGATCTTCAACAAG 240  
Db 571 GTACACGCGAGGTCCTGGGGCTGGGCATCAACGGCAAAAGTTTGTGAGATCTTCAACAAG 630  
  
Qy 241 AGNACCAGAGAAATTCGCGCTCAAAATGCTTCAGGACTGCCCCCAAGGCGCGAGGAG 300  
Db 631 AGNACCAGAGAAATTCGCGCTCAAAATGCTTCAGGACTGCCCCCAAGGCGCGAGGAG 690  
  
Qy 301 GTGGAGCTGCACGTGGCGGCTCCACGTGCGCGACATCTGACGATCTGGTGGATGTGTAC 360  
Db 691 GTGGAGCTGCACGTGGCGGCTCCACGTGCGCGACATCTGACGATCTGGTGGATGTGTAC 750  
  
Qy 361 GAGAATCTGTACGAGGAGGAAGTGCTCTGATTTGTCATGGAATTTTGGACGGTGGGA 420  
Db 751 GAGAATCTGTACGAGGAGGAAGTGCTCTGATTTGTCATGGAATTTTGGACGGTGGGA 810  
  
Qy 421 GAACTCTTTAGCGAATTCAGGATTCAGGAGGACGAGCATTCACAGAAGAGAGCATCC 480  
Db 811 GAACTCTTTAGCGAATTCAGGATTCAGGAGGACGAGCATTCACAGAAGAGAGCATCC 870  
  
Qy 481 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCATCAACATTTGCCCAT 540  
Db 871 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCATCAACATTTGCCCAT 930  
  
Qy 541 CGGATGTCAAGCTGAGAAATCTTTATACACCTTCCAAAAGGCCCAACGGCCATCTCTGAAA 600  
Db 931 CGGATGTCAAGCTGAGAAATCTTTATACACCTTCCAAAAGGCCCAACGGCCATCTCTGAAA 990  
  
Qy 601 CTCACTGACTTTGGCTTTCAGAGAAACACCGAGCCACAACTCTTTGACCACTCTCTTGT 660  
Db 991 CTCACTGACTTTGGCTTTCAGAGAAACACCGAGCCACAACTCTTTGACCACTCTCTTGT 1050  
  
Qy 661 TATACACCGTACTATGTGGCTCCAGAAAGTGCTGGGTCCAGAGAGTATGACAAATCTCTGT 720  
Db 1051 TATACACCGTACTATGTGGCTCCAGAAAGTGCTGGGTCCAGAGAGTATGACAAATCTCTGT 1110  
  
Qy 721 GACATGTGCTCCCTGGGTGTACATGATACATCTGCTGTGTGGGTATCCCCCTTTCTAC 780  
Db 1111 GACATGTGCTCCCTGGGTGTACATGATACATCTGCTGTGTGGGTATCCCCCTTTCTAC 1170  
  
Qy 781 TCCAAACACGCGCTTGCATCTCTCCGGGATGAAGACTCGCATCCGAATGGGCGAGTAT 840  
Db 1171 TCCAAACACGCGCTTGCATCTCTCCGGGATGAAGACTCGCATCCGAATGGGCGAGTAT 1230  
  
Qy 841 GAAATTTCCCAACCCAGAAATGGTCAGAAAGTATCAGAGGAAAGTGATGCTCATTCGGAAT 900

Db 1231 GAATTTCCCAACCCAGAAATGGTCAGAAATATCAGAGAAAGTGAAGATGCTCATTCGGAAT 1290  
Qy 901 CTGCTGAAAACAGAGCCCAACCCAGAGAAATGACCATCACCGAGTTTATGAACCAACCTTGG 960  
Db 1291 CTGCTGAAAACAGAGCCCAACCCAGAGAAATGACCATCACCGAGTTTATGAACCAACCTTGG 1350  
Qy 961 ATCATGCAATCAAAAGTCTCCTCAACCCCACTGCACACCAACCGGGTCTTGAAGGAG 1020  
Db 1351 ATCATGCAATCAAAAGTCTCCTCAACCCCACTGCACACCAACCGGGTCTTGAAGGAG 1410  
Qy 1021 GACAAGGAGCGGTGGAGGATGTCAAGGAGGAGATCACAGTGCCTTGGCCCAATCGCG 1080  
Db 1411 GACAAGGAGCGGTGGAGGATGTCAAGGAGGAGATCACAGTGCCTTGGCCCAATCGCG 1470  
Qy 1081 GTTGACTACAGCAGATCAAGATAAAAGATTGAAGATGATCCAAACCTCTGCTGCTG 1140  
Db 1471 GTTGACTACAGCAGATCAAGATAAAAGATTGAAGATGATCCAAACCTCTGCTGCTG 1530  
Qy 1141 AGAGGCGGAAGAAAGCTCGGCGCTGGAGGCTGCGGCTCTGGCCCACTGA 1191  
Db 1531 AGAGGCGGAAGAAAGCTCGGCGCTGGAGGCTGCGGCTCTGGCCCACTGA 1581  
  
RESULT 6  
ABK84657  
ID ABK84657 standard; cDNA; 1336 BP.  
XX  
AC ABK84657;  
XX  
DT 14-AUG-2002 (first entry)  
XX  
DE Human cDNA differentially expressed in granulocytic cells #1228.  
XX  
KW Human; ss; granulocytic cell; DNA chip; bacterial infection;  
KW viral infection; parasitic infection; protozoal infection;  
KW fungal infection; sterile inflammatory disease; psoriasis;  
KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;  
KW cardiac reperfusion injury; renal reperfusion injury; ARDS;  
KW adult respiratory distress syndrome; inflammatory bowel disease;  
KW Crohn's disease; ulcerative colitis; periodontal disease;  
KW granulocyte activation; chronic inflammation; allergy.  
XX  
OS Homo sapiens.  
XX  
PN WO200228999-A2.  
XX  
PD 11-APR-2002.  
XX  
PF 03-OCT-2001; 2001WO-US030821.  
XX  
PR 03-OCT-2000; 2000US-0237189P.  
XX  
PA (GENE-) GENE LOGIC INC.  
XX  
PI Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;  
XX  
DR WPI; 2002-435328/46.  
XX  
PT Detecting granulocyte activation by detecting differential expression of  
PT genes associated with granulocyte activation, which serves as diagnostic  
PT markers that is useful for monitoring disease states and drug toxicity.  
XX  
PS Claim 1; SEQ ID NO 1228; 114pp; English.  
XX  
CC The invention relates to detecting (M1) granulocyte (GC) activation  
CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by  
CC DNA chip analysis as given in the specification, and comparing the  
CC expression level to an expression level in an unactivated GC, where  
CC differential expression of Gs is indicative of GCA. Also included are  
CC modulating (M2) GA by contacting GC with an agent that alters the  
CC expression of at least one gene in Gs; (2) screening (M3) for an agent  
CC capable of modulating GCA or an inflammation (especially chronic) in a















CC	psychoneuroendocrinimmune gene expressed sequence tag. Note the
CC	specificatio mentions SEQ ID NO of up to 3314 but only sequences up to
CC	SEQ ID NO 1829 are provided.
XX	
SQ	Sequence 1113 BP; 276 A; 343 C; 286 G; 208 T; 0 U; 0 Other;
Query Match 88.0%; Score 1048.4; DB 14; Length 1113;	
Best Local Similarity 99.94; Pred. No. 4.1e-228;	
Matches 1049; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	1 TCCAGGGCCAGAGCCGCGGTGCGCTTCCCGCCCGCCCGCGCGCGAGCCCCC 60
DB	
QY	13 TCCAGGGCCAGAGCCGCGGTGCGCTTCCCGCCCGCGCGCGCGAGCCCCC 72
DB	
QY	61 ACCCTGCTCCGCGCACCCCGCGGCGAGCGCGCGCGCGCGCGAGTTCGCG 120
DB	
QY	73 ACCCTGCTCCGCGCACCCCGCGGCGAGCGCGCGCGCGCGCGAGTTCGCG 132
DB	
QY	121 CAGTTCACGTCAAGTCCGCGCTGCAGATCAAGAGAACGCCATCATCGATGACTACAAG 180
DB	
QY	133 CAGTTCACGTCAAGTCCGCGCTGCAGATCAAGAGAACGCCATCATCGATGACTACAAG 192
DB	
QY	181 GTCAACAGCAGGTCCTGGGGCTGGGCATCAACGGCAAGTCTTGCAGATCTTCAACAAG 240
DB	
QY	193 GTCAACAGCAGGTCCTGGGGCTGGGCATCAACGGCAAGTCTTGCAGATCTTCAACAAG 252
DB	
QY	241 AGGACCCAGAGAAATTCGGCCTCAAAATGCTTCAAGACTGCCCCCAAGGCCCGCAGGGAG 300
DB	
QY	253 AGGACCCAGAGAAATTCGGCCTCAAAATGCTTCAAGACTGCCCCCAAGGCCCGCAGGGAG 312
DB	
QY	301 GTGGAGCTGACTGGCGGGCTCCAGTGGCGGCACATCTAGCGATCGTGGATGTGTAC 360
DB	
QY	313 GTGGAGCTGACTGGCGGGCTCCAGTGGCGGCACATCTAGCGATCGTGGATGTGTAC 372
DB	
QY	361 GAGAACTGTACGAGGAGGAAGTGCCTGATGTCATGGAATGTTTGGACGGTGA 420
DB	
QY	373 GAGAACTGTACGAGGAGGAAGTGCCTGATGTCATGGAATGTTTGGACGGTGA 432
DB	
QY	421 GAACCTTTTACCGGAATCCAGGATTCGAGGAGACAGGCGATTCACAGAAAGAGAGCATCC 480
DB	
QY	433 GAACCTTTTACCGGAATCCAGGATTCGAGGAGACAGGCGATTCACAGAAAGAGAGCATCC 492
DB	
QY	481 GAATCATGAGAGCATCGGTGAGGCCATCAGTATCTGCATTCATCAATCAACATTCGCCAT 540
DB	
QY	493 GAATCATGAGAGCATCGGTGAGGCCATCAGTATCTGCATTCATCAATCAACATTCGCCAT 552
DB	
QY	541 CGGGATCTCAAGCTGAGAAATCTTTATACACCTTCCAAAAGGCCCAACGCCATCTCGAAA 600
DB	
QY	553 CGGGATCTCAAGCTGAGAAATCTTTATACACCTTCCAAAAGGCCCAACGCCATCTCGAAA 612
DB	
QY	601 CTCACTGACTTTGGCTTTGCCAAGGAAACCAACGAGCCACAACCTTTTGGACCATCTCTGT 660
DB	
QY	613 CTCACTGACTTTGGCTTTGCCAAGGAAACCAACGAGCCACAACCTTTTGGACCATCTCTGT 672
DB	
QY	661 TATACCGTACTATGTGGCTCCAGAGAGTGTGGTCCAGAGAGTATGACAGTCTCTGT 720
DB	
QY	673 TATACCGTACTATGTGGCTCCAGAGAGTGTGGTCCAGAGAGTATGACAGTCTCTGT 732
DB	
QY	721 GACATGTGGTCCCTGGGTGTTCATCATGTACATCTCTGTGTGGGTATCCCCCTTCTAC 780
DB	
QY	733 GACATGTGGTCCCTGGGTGTTCATCATGTACATCTCTGTGTGGGTATCCCCCTTCTAC 792
DB	
QY	781 TCCAAACAGCGCTTGGCATCTCTCCGGGCGATGAAGACTGCGATCCGAATGGGCGAGTAT 840
DB	
QY	793 TCCAAACAGCGCTTGGCATCTCTCCGGGCGATGAAGACTGCGATCCGAATGGGCGAGTAT 852
DB	
QY	841 GAATTTCCCAACCCAGAAATGTGACAGAGTATCAGAGAGAGTGAAGTCTCATTCGGAAT 900
DB	
QY	853 GAATTTCCCAACCCAGAAATGTGACAGAGTATCAGAGAGAGTGAAGTCTCATTCGGAAT 912
DB	
QY	901 CTGCTGAAACAGAGGCCACCCAGAGAGATGACCATCAACCGAGTTTATGAACCAACCTTGG 960
DB	
QY	913 CTGCTGAAACAGAGGCCACCCAGAGAGATGACCATCAACCGAGTTTATGAACCAACCTTGG 972
DB	

QY	961 ATCATGCAATCAACAAAGTCTCTCAAAACCCCACTCTCACACCAAGCCGGTCTCTGAAGGAG 1020
DB	
QY	973 ATCATGCAATCAACAAAGTCTCTCAAAACCCCACTCTCACACCAAGCCGGTCTCTGAAGGAG 1032
DB	
QY	1021 GACAAGGAGCGGTGGGAGGATGTCAAGGAG 1050
DB	
QY	1033 GACAAGGAGCGGTGGGAGGATGTCAAGGAG 1062
DB	
RESULT 12	
ADP87584	
ID	ADP87584 standard; DNA; 1128 BP.
XX	
AC	ADP87584;
XX	
DT	23-SEP-2004 (first entry)
XX	
DE	Human NOVX polypeptide encoding DNA, NOV3d.
XX	
KW	anorectic; antidiabetic; gene therapy; vaccine; obesity; diabetes;
KW	insulin resistance; hybridization probe; chromosome mapping;
KW	tissue typing; preventive medicine; pharmacogenomics; NOVX; human; gene;
KW	ds.
OS	Homo sapiens.
XX	
PN	WO2004056961-A2.
XX	
PD	08-JUL-2004.
XX	
PF	27-OCT-2003; 2003WO-US034114.
XX	
PR	25-OCT-2002; 2002US-0421239P.
PR	28-OCT-2002; 2002US-0421700P.
PR	31-OCT-2002; 2002US-0422776P.
PR	13-NOV-2002; 2002US-0426197P.
PR	20-DEC-2002; 2002US-0435498P.
PR	20-DEC-2002; 2002US-0435510P.
PR	20-DEC-2002; 2002US-0435568P.
PR	21-MAR-2003; 2003US-0456812P.
XX	
PA	(CURA-) CURAGEN CORP.
XX	
PI	Berghs C, Catterton E, Ellerman K, Ort T, Rieger D, Chaudhuri A;
XX	
DR	WPI; 2004-500293/47.
XX	P-PSDB; ADP87585.
PT	New NOVX nucleic acid molecules and polypeptides useful for preventing or
PT	treating NOVX-associated disorders, e.g. diabetes, insulin resistance or
PT	obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX	
PS	Claim 1; SEQ ID NO 39; 570pp; English.
XX	
CC	The invention relates to a novel isolated nucleic acid molecule
CC	comprising any of the nucleotide sequences (e.g. 3634, 2127 or 2120 base
CC	pairs) fully defined in the specification; or encodes any of the amino
CC	acid sequences (e.g. 698, 702 or 709 amino acids) fully defined in the
CC	specification. The invention further comprises: an isolated polypeptide
CC	comprising any of the amino acid sequences cited above; a method for
CC	identifying compounds that modulate target polypeptide activity; an
CC	antibody that immunospecifically binds to the target polypeptide; where
CC	the target polypeptide comprises any of the above-mentioned amino acid
CC	sequences, an amino acid sequence that is at least 95% identical to the
CC	above amino acid sequences, an amino acid sequence of at least one domain
CC	of the above-mentioned amino acid sequences, or an amino acid sequence
CC	that is at least 95% identical to the domain of the above amino acid
CC	sequences; a method for identifying a potential therapeutic agent for use
CC	in treatment of a pathology, where the pathology is related to aberrant
CC	expression or aberrant physiological interactions of a target polypeptide
CC	; and a method of screening for a modulator of activity of or of latency
CC	or predisposition to a pathology associated with a target polypeptide.







PT New composition comprising polynucleotide probes, useful as array  
PT elements in a microarray for monitoring the expression of target  
PT polynucleotides or purifying a subpopulation of mRNAs, cDNA, or genomic  
PT fragments.

XX Claim 6; SEQ ID NO 1415; 73pp; English.

XX The invention relates to a composition of polynucleotide probes  
CC comprising first polynucleotide probes comprising at least a portion of a  
CC gene encoding a receptor-like polypeptide, second polynucleotide probes  
CC comprising at least a portion of a gene encoding a transducing  
CC polypeptide and third polynucleotide probes comprising at least a portion  
CC of a gene encoding an effector-like polypeptide. The probes of the  
CC composition are useful as array elements in a microarray for monitoring  
CC the expression of target polynucleotides. The microarray is useful in the  
CC diagnosis and treatment of cancer, an immunopathology or a  
CC neuropathology. It can also be used for drug discovery and development,  
CC toxicological and carcinogenicity studies, forensics or pharmacogenomics.  
CC Microarrays can also be used for monitoring the progression of diseases  
CC that may be associated with the altered expression of signalling pathway  
CC polypeptides. The composition can also be used to purify a subpopulation  
CC of mRNAs, cDNAs, or genomic fragments in a sample. The expression profile  
CC is also useful for the diagnosis and treatment of cancer, e.g. cancers of  
CC the adrenal gland, bladder, bone, bone marrow, brain, breast or cervix,  
CC an immunopathology, e.g. AIDS, diabetes, pancreatitis, osteoporosis or  
CC ulcerative colitis, or a neuropathology, e.g. dementia, amnesia,  
CC epilepsy, Alzheimer's disease or depression. This sequence represents a  
CC human polynucleotide probe of the invention. Note: The sequence data for  
CC this patent did not form part of the printed specification but was  
CC obtained in electronic format directly from USPTO at  
CC seqdata.uspto.gov/sequence.html.

XX SQ Sequence 2258 BP; 496 A; 711 C; 618 G; 433 T; 0 U; 0 Other;

Query Match 88.0%; Score 1048.4; DB 12; Length 2258;  
Best Local Similarity 99.9%; Pred. No. 5e-228;  
Matches 1049; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCAGGGCCAGAGCCCGCGGTGCCGTTCCCGCCCGCGCCCGCGCGCGCGCGCC 60  
Db 391 TCCAGGGCCAGAGCCCGCGGTGCCGTTCCCGCCCGCGCCCGCGCGCGCGCC 450

Qy 61 ACCCTCGCTGCGCAGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120  
Db 451 ACCCTCGCTGCGCAGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 510

Qy 121 CAGTTCACGTCACAGTCCGGCTCCAGATCAAGAAAGACGCCATCATCGATGACTACAAG 180  
Db 511 CAGTTCACGTCACAGTCCGGCTCCAGATCAAGAAAGACGCCATCATCGATGACTACAAG 570

Qy 181 GTACACGACCGAGTCTGGGGCTGGGCATCAACGGCAAAAGTTTGGCAGATCTTCAACAAG 240  
Db 571 GTACACGACCGAGTCTGGGGCTGGGCATCAACGGCAAAAGTTTGGCAGATCTTCAACAAG 630

Qy 241 AGGACCCAGAGAAATTCGCCCTCAAAATGCTTCAGGACTGCCCAAGGCCCGCAGGGAG 300  
Db 631 AGGACCCAGAGAAATTCGCCCTCAAAATGCTTCAGGACTGCCCAAGGCCCGCAGGGAG 690

Qy 301 GTGGAGCTGCATCGCGGGCCCTCCAGTGGCCCGCACATCGTACGGATCGTGGATGTGTAC 360  
Db 691 GTGGAGCTGCATCGCGGGCCCTCCAGTGGCCCGCACATCGTACGGATCGTGGATGTGTAC 750

Qy 361 GAGAATCTGTACGAGGAGGAAGTGCCTGCTGATTGTTCATGGAATGTTGGACGGTGA 420  
Db 751 GAGAATCTGTACGAGGAGGAAGTGCCTGCTGATTGTTCATGGAATGTTGGACGGTGA 810

Qy 421 GAACCTTTTAGCGGAATTCAGGATCGAGGACACAGGATTCACAGAAAGAGAGCATCC 480  
Db 811 GAACCTTTTAGCGGAATTCAGGATCGAGGACACAGGATTCACAGAAAGAGAGCATCC 870

Qy 481 GAAATCATGAAGACATCGGTGAGGCCATCCAGTATCTGCATTCATCAATCAACATTCGCCAT 540  
Db 871 GAAATCATGAAGACATCGGTGAGGCCATCCAGTATCTGCATTCATCAATCAACATTCGCCAT 930

Search completed: June 19, 2006, 16:04:09  
Job time : 850 secs

Qy 541 CGGGATGTCAAGCCTGAGAAATCTTTATACACCTCCAAAAGGCCCAACGCCATCTCTGAAA 600  
Db 931 CGGGATGTCAAGCCTGAGAAATCTTTATACACCTCCAAAAGGCCCAACGCCATCTCTGAAA 990

Qy 601 CTCACATGACTTTGGCTTCCAGAGGAACACACAGCAGCAACATCTTTTGACCATCTCCTTGT 660  
Db 991 CTCACATGACTTTGGCTTCCAGAGGAACACACAGCAGCAACATCTTTTGACCATCTCCTTGT 1050

Qy 661 TATACACCGGTACTATGTGGCTCCAGAAAGTCTGGTCCAGAGAAAGTATGACAAAGTCTCTGT 720  
Db 1051 TATACACCGGTACTATGTGGCTCCAGAAAGTCTGGTCCAGAGAAAGTATGACAAAGTCTCTGT 1110

Qy 721 GACATGTGCTCCCTGGGTGTATCATGTATCATCTCTGTGTGGGTATCCCCCTTCTTAC 780  
Db 1111 GACATGTGCTCCCTGGGTGTATCATGTATCATCTCTGTGTGGGTATCCCCCTTCTTAC 1170

Qy 781 TCCAAACACGGCCCTTCCCATCTCTCCGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 840  
Db 1171 TCCAAACACGGCCCTTCCCATCTCTCCGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 1230

Qy 841 GAAATTTCCCAACCCAGAAATGGTCCAGAAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT 900  
Db 1231 GAAATTTCCCAACCCAGAAATGGTCCAGAAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT 1290

Qy 901 CTGCTGAAAACAGAGCCCGCAGAGAAATGACCATCAGGATTTATGAACACCCCTTGG 960  
Db 1291 CTGCTGAAAACAGAGCCCGCAGAGAAATGACCATCAGGATTTATGAACACCCCTTGG 1350

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Qy 1021 GACAAGGAGCGGTGGGAGGATGTAAGGAG 1050  
Db 1411 GACAAGGAGCGGTGGGAGGATGTAAGGAG 1440

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2006, 15:52:45 ; Search time 6434 Seconds  
(without alignments)  
10351.247 Million cell updates/sec

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Perfect score: 1191

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.\*

1: gb\_est1.\*  
2: gb\_est3.\*  
3: gb\_est4.\*  
4: gb\_est5.\*  
5: gb\_est6.\*  
6: gb\_hic.\*  
7: gb\_est2.\*  
8: gb\_est7.\*  
9: gb\_est8.\*  
10: gb\_est9.\*  
11: gb\_gss1.\*  
12: gb\_gss2.\*  
13: gb\_gss3.\*  
14: gb\_gss4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	928.4	78.0	2674	6 AK155171	Mus muscu
2	894.8	75.1	901	8 CR980921	CR980921
3	780	65.5	780	14 AY410229	AY410229 Homo sapi
4	755.6	63.4	850	9 DN107605	DN107605 1105067 M
5	742.6	62.4	941	3 BG884713	BG884713 AGENCOURT
6	737.6	61.9	785	2 BG397545	BG397545 602439376
7	715	60.0	726	8 CN431763	CN431763 170006001
8	710	59.6	710	10 DR423458	DR423458 nav26d01.
9	710	59.6	756	8 CV804995	CV804995 AGENCOURT
10	688	57.8	720	2 BG779875	BG779875 602667370
11	678	56.9	902	10 DV928789	DV928789 LB03014.C
12	663.2	55.7	780	14 AY410231	AY410231 Mus muscu
13	660.4	55.4	855	8 CO399284	CO399284 AGENCOURT
14	652.6	54.8	1048	2 BG106843	BG106843 60291408
15	652.2	54.8	776	3 BU609266	BU609266 UI-M-FRO-
16	649.8	54.6	842	5 CF617043	CF617043 AGENCOURT
17	646.4	54.3	654	8 CN431764	CN431764 170006001
18	644.6	54.1	803	5 CF725030	CF725030 UI-M-GZO-
19	641.6	53.9	651	4 CB043982	NISC_gc01

20	641	53.8	858	8	CO394436	AGENCOURT
21	637.6	53.5	945	2	BG421869	602449607
22	636.6	53.5	825	7	BP309820	601892475
23	635.4	53.4	751	4	CB169658	RUC603000
24	634.4	53.3	846	2	BG480613	602527051
25	624.8	52.5	827	9	DN284271	1184539 M
26	620	52.1	778	8	CO246458	AGENCOURT
27	615.4	51.7	909	7	BE876507	601486252
28	613.4	51.5	696	1	AI478890	tm25b05.x
29	611.2	51.3	752	8	CK974173	4104800 B
30	604.6	50.8	728	5	CF725542	UI-M-GZO-
31	604.4	50.7	727	8	CV783919	UI-M-HY0P
32	601.2	50.5	642	7	BE280175	601158383
33	596.2	50.1	875	5	CF582482	AGENCOURT
34	594.2	49.9	915	3	BO964944	AGENCOURT
35	591.4	49.7	690	7	AW918725	EST350029
36	590.8	49.6	675	3	BU671169	NISC_lr05
37	585.6	49.2	729	9	DN933930	AGENCOURT
38	585.2	49.1	739	2	BI077614	602871715
39	583.6	49.0	690	10	DY113286	000311BSP
40	582	48.9	663	10	DT824579	LB00234.C
41	581.6	48.8	764	2	BI150810	602914708
42	579.8	48.7	1182	9	DN666480	CFW32-D05
43	576.6	48.4	789	9	DN872742	nao22b02.
44	574.8	48.3	648	7	AW071750	ws55b11.x
45	573.6	48.2	653	10	DT828222	LB00256.C

## ALIGNMENTS

RESULT 1	AK155171	2674 bp	mRNA	linear	HTC 21-SEP-2005
LOCUS	AK155171				
DEFINITION	Mus musculus NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F630205L24 product:MAP kinase-activated protein kinase 2, full insert sequence.				
ACCESSION	AK155171	1	GI:74199084		
VERSION	AK155171				
KEYWORDS	HTC; CAP trapper.				
SOURCE	Mus musculus				
ORGANISM	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.				
REFERENCE	1 Carninci, P. and Hayashizaki, Y.				
AUTHORS	High-efficiency full-length cDNA cloning				
TITLE	Meth. Enzymol. 303, 19-44 (1999)				
JOURNAL	10349636				
PUBMED	2				
REFERENCE	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.				
AUTHORS	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
TITLE	Genome Res. 10 (10), 1617-1630 (2000)				
JOURNAL	11042159				
PUBMED	3				
REFERENCE	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Tashiro, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.				
AUTHORS	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer				
TITLE	Genome Res. 10 (11), 1757-1771 (2000)				
JOURNAL	11076861				
PUBMED	4				
REFERENCE	Kawai, J., Shingawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I.,				



Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kuchiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesole, G., Quackenbush, J., Schriml, L.M., Staebli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barah, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kaniya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ringwald, M., Rodriquez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyooka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawajiri, H., Kotsuiki, S. and Hayashizaki, Y.

RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium

Functional annotation of a full-length mouse cDNA collection  
Nature 409 (6821), 685-690 (2001)  
11217851

5

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaide, I., Osato, N., Saito, R., Suzuki, H., Yananaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusci, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawajiri, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.

FANTOM Consortium

Analysis of the mouse transcriptome based on functional annotation  
Of 60,770 full-length cDNAs  
Nature 420 (6915), 563-573 (2002)  
12466851

6

Meada, N., Oyama, R., Ravasi, T., Lenhard, B., Wells, C., Kodzius, R., Shimokawa, K., Bajic, V.B., Brenner, S.E., Batalov, S., Forrest, A.R., Zavolan, M., Davis, M.J., Wilming, L.G., Aidinis, V., Allen, J.E., Bansal-Impombato, A., Apweiler, R., Aturaliya, R.N., Bailey, T.L., Banaei, M., Baxter, L., Beisel, K.W., Bersano, T., Bono, H., Chalk, A.M., Chiu, K.P., Choudhary, V., Christoffels, A., Clutterbuck, D.R., Crowe, M.L., Dalla, E., Dalrymple, B.P., de Bono, B., Della Gatta, G., di Bernardo, D., Down, T., Engstrom, P., Fagiolini, M., Faulkner, G., Fletcher, C.F., Fukushima, T., Furuno, M., Futaki, S., Gariboldi, M., Gojobori, T., Gieger, T.R., Gojobori, T., Green, R.E., Gustincich, S., Harbers, M., Hayashi, Y., Hensch, T.K., Hirokawa, N., Hill, D., Humnicki, L., Iacono, M., Ikeo, K., Iwama, A., Ishikawa, T., Jakt, M., Kanapin, A., Katoh, M., Kawasawa, Y., Kelso, J., Kitamura, H., Kitano, H., Kollas, G., Krishnan, S.P., Kruger, A., Kummerfeld, S.K., Kurochkin, I.V., Lareau, L.F., Lazarevic, D., Lipovich, L., Liu, J., Lluni, S., McWilliam, S., Madan Babu, M., Madera, M., Marchionni, L., Matsuda, H., Matsuzawa, S., Miki, H., Mignone, F., Miyake, S.,

Morris, K., Mottagui-Tabar, S., Mulder, N., Nakano, N., Nakauchi, H., Ng, P., Nilsson, R., Nishiguchi, S., Nishikawa, S., Nori, P., Ohara, O., Okazaki, Y., Orlando, V., Pang, K.C., Pavan, W.J., Pavesi, G., Pesole, G., Petrovsky, N., Piazza, S., Reed, J., Reid, J.F., Ring, B.Z., Ringwald, M., Rost, B., Ruan, Y., Salzberg, S.L., Sandelin, A., Schneider, C., Schonbach, C., Sekiguchi, K., Semple, C.A., Seno, S., Sessa, L., Sheng, Y., Shibata, Y., Shimada, H., Shimada, K., Silva, D., Sinclair, B., Sperling, S., Stupka, E., Sugura, K., Sultana, R., Takenaka, Y., Taki, K., Tammoja, K., Tan, S.L., Tang, S., Taylor, M.S., Tegner, J., Teichmann, S.A., Ueda, H.R., van Nimwegen, E., Verardo, R., Wei, C.L., Yagi, K., Yamanishi, H., Zabarovsky, E., Zhu, S., Zimmer, A., Hide, W., Bult, C., Grimmond, S.M., Teasdale, R.D., Liu, E.T., Brusci, V., Quackenbush, J., Wahlestedt, C., Mattick, J.S., Hume, D.A., Kai, C., Sasaki, D., Tomaru, Y., Fukuda, S., Kanamori-Katayama, M., Suzuki, M., Aoki, J., Arakawa, T., Iida, J., Imamura, K., Itoh, M., Kato, T., Kawajiri, H., Kawagashira, N., Kawashima, T., Kojima, M., Kondo, S., Konno, H., Nakano, K., Ninomiya, N., Nishio, T., Okada, M., Plessy, C., Shibata, K., Shiraki, T., Suzuki, S., Tagami, M., Waki, K., Watabiki, A., Okamura-Oho, Y., Suzuki, H., Kawai, J. and Hayashizaki, Y.

FANTOM Consortium

The transcriptional landscape of the mammalian genome  
Science 309 (5740), 1559-1563 (2005)  
16141072

7

Katayama, S., Tomaru, Y., Kasukawa, T., Waki, K., Nakanishi, M., Nakamura, M., Nishida, H., Yap, C.C., Suzuki, M., Kawai, J., Suzuki, H., Carninci, P., Hayashizaki, Y., Wells, C., Frith, M., Ravasi, T., Pang, K.C., Hallinan, J., Mattick, J., Hume, D.A., Lipovich, L., Batalov, S., Engstrom, P.G., Mizuno, Y., Faghihi, M.A., Sandelin, A., Chalk, A.M., Mottagui-Tabar, S., Liang, Z., Lenhard, B. and Wahlestedt, C.

RIKEN Genome Research Group

Antisense transcription in the mammalian transcriptome  
Science 309 (5740), 1564-1566 (2005)  
16141073

8 (bases 1 to 2674)

Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hori, F., Iida, J., Imamura, K., Imotani, K., Itoh, M., Kanagawa, S., Kawai, J., Kojima, M., Konno, H., Murata, M., Nakamura, M., Ninomiya, N., Nishiyori, H., Nomura, K., Ohno, M., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shiraki, T., Tagami, M., Tagami, Y., Waki, K., Watabiki, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.

Please visit our web site for further details.  
URL: http://genome.gsc.riken.jp/  
URL: http://fantom.gsc.riken.jp/  
Location/Qualifiers  
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286. 11446

CDS





NotI; vector: http://www.rzpd.de/info/vectors/pQB80LSN_cloned_pic.shtml ; 1st strand cDNA was prepared from mRNA obtained from human T-Lymphocytes with a NotI - oligo(df) primer [5', GACTAGTCTAGATCGGACGGCGCCCTTTTCTTTTCTTTT 3']. Double-stranded cDNA was ligated to SalI adaptors, digested with NotI and cloned into the NotI and SalI sites of the pQB80LSN_cloned vector"		75.1%; Score 894.8; DB 8; Length 901; Best Local Similarity 99.4%; Pred. No. 2.6e-208; Matches 896; Conservative 0; Mismatches 5; Indels 0; Gaps 0;	
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Qy	163	ATCATCGATGACTACAAAGGTCACAGCCAGGTCCTGGGGCTGGGCATCAACGGCAAGTT	222
Db	1	ATCATCGATGACTACAAAGGTCACAGCCAGGTCCTGGGGCTGGGCATCAACGGCAAGTT	60
Qy	223	TTGCAGATCTTCAACAAAGAGGACCCAGGAGAAATTCGCCCTCAAAATGCTTCAGGACTGC	282
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Qy	283	CCCAAGCCCGCAGGGAGGTGGAGCTGCACCTGCGGGCCCTCCAGTGCCTCCGACATCGTA	342
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Qy	643	TCTTTGACCACTCCTTGTTATACACCGTATCATGTGGTCTCAGAAAGTGTGGGTCCAGAG	702
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Qy	763	GGGTATCCCCCTTCTACTCCAACACAGCGCTTCCCATCTCTCCGGGCATGAAGACTCGC	822
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Qy	823	ATCCGAATGGGCCAGTATGAATTTCCAAACCCAGATGGTTCAGAAATATCAGAGGAAGTG	882
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Qy	1003	AGCCGGGTCTGGAAGGAGGACCAAGCGGTGGAGGATGTCAAGGAGGAGATGACCAAGT	1062
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Qy	1063	G	1063
Db	901	G	901
RESULT 3			
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LOCUS	Homo sapiens MAPKAPK2 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.		
DEFINITION			
ACCESSION	AY410229		
VERSION	AY410229.1	GI:39766197	
KEYWORDS	GSS.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE			
AUTHORS			
1 (bases 1 to 780)			
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.			
TITLE			
Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios			
JOURNAL			
PUBMED			
2 (bases 1 to 780)			
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.			
TITLE			
Direct Submission			
JOURNAL			
COMMENT			
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA This sequence was made by sequencing genomic exons and ordering them based on alignment.			
FEATURES			
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Query Match 65.5%; Score 780; DB 14; Length 780;			
Best Local Similarity 100.0%; Pred. No. 3.7e-180;			
Matches 780; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	268	ATGCTTCAGGACTGCCCAAGGCCCGCAGGAGTGGAGCTGCACCTGGCGGGCTCCCGAG	327
Db	1	ATGCTTCAGGACTGCCCAAGGCCCGCAGGAGTGGAGCTGCACCTGGCGGGCTCCCGAG	60
Qy	328	TGCCCCACATCGTACGGATCGTGGATGTGTACGAGAACTGTACGAGGAGGAAGTGC	387
Db	61	TGCCCCACATCGTACGGATCGTGGATGTGTACGAGAACTGTACGAGGAGGAAGTGC	120
Qy	388	CTGCTGATTGTATGGAATGTTTGGACGGTGGAGAACTCTTTAGCCGAATCCAGGATCGA	447
Db	121	CTGCTGATTGTATGGAATGTTTGGACGGTGGAGAACTCTTTAGCCGAATCCAGGATCGA	180
Qy	448	GGAGACCGGATTCACAGAAAGAGGATCCGAAATCATGAAGAGCATCGGTGAGGCC	507
Db	181	GGAGACCGGATTCACAGAAAGAGGATCCGAAATCATGAAGAGCATCGGTGAGGCC	240
Qy	508	ATCCAGTATCTGCATTCAATCAACATTGCCCATCGGATGTCAAGCCTGAGAAATCTCTTA	567
Db	241	ATCCAGTATCTGCATTCAATCAACATTGCCCATCGGATGTCAAGCCTGAGAAATCTCTTA	300
Qy	568	TACACCTCCAAAGGGCCCAACGCCATCTCTGAAACTCACTGACTTTGGCTTTGCCAAGGAA	627

Db 301 TACACCTCCAAAGGCCCAAGCCATCTGAAACTCACTGACTTTGGCTTTGGCCAAAGAA 360  
QY 628 ACCACCGCCCAACTCTTTGACCACTCCTTGTGTATATACACCGTACTATGTGGCTCCAGAA 687  
Db 361 ACCACCGCCCAACTCTTTGACCACTCCTTGTGTATATACACCGTACTATGTGGCTCCAGAA 420  
QY 688 GTGCTGGGTCCAGAGAAATGATGACAAAGTCCCTGTGTGACATGTGCTCCTGGGTGTATCATG 747  
Db 421 GTGCTGGGTCCAGAGAAATGATGACAAAGTCCCTGTGTGACATGTGCTCCTGGGTGTATCATG 480  
QY 748 TACATCTGTGTGTGGGTATCCCGCTTCTACTCTCAACACAGCGCTTGGCCATCTCTCCG 807  
Db 481 TACATCTGTGTGTGGGTATCCCGCTTCTACTCTCAACACAGCGCTTGGCCATCTCTCCG 540  
QY 808 GGCATGAAGACTCCGATCCGAATGGCCAGTATGAATTTCCCAACCCAGAGTGTGAGAA 867  
Db 541 GGCATGAAGACTCCGATCCGAATGGCCAGTATGAATTTCCCAACCCAGAGTGTGAGAA 600  
QY 868 GTATCAGAGGAAGTGAAGTCTCATTCGGGAATCTGTGAAACAGAGCCCAACCCAGAGA 927  
Db 601 GTATCAGAGGAAGTGAAGTCTCATTCGGGAATCTGTGAAACAGAGCCCAACCCAGAGA 660  
QY 928 ATGACCATFACCGAGTTTATGAACACACCTTTGGATCATGCAATCAACAAAGGTCCCTCAA 987  
Db 661 ATGACCATFACCGAGTTTATGAACACACCTTTGGATCATGCAATCAACAAAGGTCCCTCAA 720  
QY 988 ACCCACTGCACACCGCGGTCTGAAGAGACAGAGCGGTGGGAGATGTCAAG 1047  
Db 721 ACCCACTGCACACCGCGGTCTGAAGAGACAGAGCGGTGGGAGATGTCAAG 780

## RESULT 4

LOCUS DNI07605 850 bp mRNA linear EST 14-FEB-2005  
DEFINITION 1105067 MARC 4PTG Sus scrofa cDNA 5', mRNA sequence.

DNI07605

VERSION DNI07605.1 GI:59782868

KEYWORDS EST.

SOURCE Sus scrofa (pig)

ORGANISM Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;  
Sus.

REFERENCE 1 (bases 1 to 850)

Smith, T.P.L., Breking, B.A., Ford, J.J., Vallet, J.L., Wise, T.A.,  
Noneman, D.J., Wray, J.E. and Keele, J.W.  
Porcine EST collection using a normalized library constructed from  
embryos representing early developmental stages

Unpublished (2003)

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called with phred v0.020425.c and  
trimmed with the aid of the trim\_alt option. Vector identified with  
cross\_match v0.990329.

Plate: HHY8003 row: B column: 15

Seq primer: GTAATACGACTCACTATAGG.

Location/Qualifiers

1. .850

/organism="Sus scrofa"

/mol\_type="mRNA"

/db\_xref="taxon:9823"

/tissue\_type="pooled"

/lab\_host="DH10B"

/clone\_lib="MARC 4PTG"

/note="Vector: pCDNA3.1; Site\_1: EcoRI; Site\_2: NotI;  
Library made with combined RNA from day-10, day-15,  
day-15, day-25, and day-30 whole embryos."

## ORIGIN

Query Match 63.4%; Score 755.6; DB 9; Length 850;  
Best Local Similarity 93.1%; Pred. No. 3.7e-174;  
Matches 791; Conservative 0; Mismatches 59; Indels 0; Gaps 0;  
QY 153 GAAGAAGCCCATCATCGATGACTACAAGGTCAACAGCCAGGTCTCTGGGTGGCATCAA 212  
Db 1 GAAGAAGCCCATCATCGATGACTACAAGGTCAACAGCCAGGTCTCTGGGTGGCATCAA 60  
QY 213 CGGAAAGTTTTCAGATCTTCAACAGAGACCAGAGAAATTCGCCCTCAAAATGCT 272  
Db 61 CGGAAAGTTTTCAGATCTTCAACAGAGACCAGAGAAATTCGCCCTCAAAATGCT 120  
QY 273 TCAGGACTGCCCAAGGCCCGCAGGGAGGTGGAGTGCACCTGGCGGCTCTCCAGTGGCC 332  
Db 121 TCAGGACTGTCCCAAGGCCCGCAGGGAGGTGGAGTGCACCTGGCGGCTCTCCAGTGGCC 180  
QY 333 GCACATCGTACGGATCGTGTACGAGAAATCTGTACGAGGGAGGAGTGCCTGCT 392  
Db 181 ACACATCGTGGATCGTGACGTCTATGAGAACCTGTACGCGGGAGGAGTGCCTACT 240  
QY 393 GATTGTTCATGGAATGTTTGGACCGGTGGAGAACTCTTTAGCCGAATCCAGGATCGAGAGA 452  
Db 241 GATCGTCATGGAGTGTGTGGATGGTGGAGAACTCTTTAGCCGAATCCAGGACCGAGAGA 300  
QY 453 CCAGGCATTCAAGAAAGAGAGCATCCGAAATCATGAAGAGCATCGTGTAGGGCCATCCA 512  
Db 301 CCAAGCGTTCAAGAAAGAGAGCATCAGAAATCATGAAGAGCATTTGTGTAGGGCCATCCA 360  
QY 513 GTATCTGATCAATCAACATTTGCCCATCGGGATGTCAAGCCTGAGAAATCTTTATACAC 572  
Db 361 GTATTTGCACTCAATCAACATTTGCTCATCGAGAGCTCAAGCCTGAGAAATCTTTGTACAC 420  
QY 573 CTCCAAAGGCCCAAGCCCATCTGAAACTCAGTACTTTGGCTTTGCCAAGGAAACAC 632  
Db 421 CTCCAAAGGCCCAAGCCCATCTGAAACTCAGTACTTTGGCTTTGCCAAGGAAACAC 480  
QY 633 CAGCCACAATCTTTGACCACTCTTGTATTATACACCGTACTATGTGGCTCCAGAAAGTGT 692  
Db 481 CAGCCACAATCTACTGACCACTCCCTGTTACAGCCGTACTATGTGGCTCCAGAAAGTGT 540  
QY 693 GGGTCCAGAGAAGTATGACAAAGTCTGTGTGACATGTGGTCTCTGGGTGTCAATGTATACAT 752  
Db 541 GGGCCCGCAGAAAGTATGACAAAGTCTGTGTGACATGTGGTCTCTGGGTGTCAATGTATACAT 600  
QY 753 CTGTCTGTGGGTATCCCCCTTCTACTCCAAACCGGCTTGGCATCTCTCCGGGCAT 812  
Db 601 CTGTCTGTGGGTATCCCCCTTCTACTCCAAACCGGCTTGGCATCTCTCCGGGCAT 660  
QY 813 GAAGACTCGCATCCGAATGGCCAGTATGAATTTCCCAACCCAGAAATGGTCAAGATATC 872  
Db 661 GAAGACTCGCATCCGAATGGCCAGTATGAATTTCCCAACCCAGAAATGGTCAAGATATC 720  
QY 873 AGAGGAAGTGAAGATGCTCATTCGGAAATCTGTGTGAAACAGAGCCCAACCCAGAGAAATGAC 932  
Db 721 AGAAGAAGTGAAGATGCTCATCCGGAACCTGTCTGAAGACAGAGCCCAACCCAGAGATGAC 780  
QY 933 CATCAGCGAGTTTATGAAACCAACCTTGGATCATGCAATCAAGAGTGCCTCTCAAAACCC 992  
Db 781 CATCAGCGAGTTTATGAAACCAACCTTGGATCATGCAATCAAGAGTGCCTCTCAAAACCC 840  
QY 993 ACTGCACACC 1002  
Db 841 ACTGCACACC 850

## RESULT 5

BQ884713

LOCUS

DEFINITION

BQ884713

ACCESSION

VERSION

BQ884713 941 bp mRNA linear EST 16-AUG-2002  
AGENCOURT\_8747447 NIH\_MGC\_130 Mus musculus cDNA clone IMAGE:6336305  
5', mRNA sequence.  
BQ884713  
BQ884713.1 GI:22276731

```

KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Mus musculus
EST.
1
(bases 1 to 941)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Mark Maconochie, Ph.D. and Nancy L. Freeman,
Ph.D.
CDNA Library Preparation: ResGen, Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L18M13800 row: b column: 18
High quality sequence stop: 700.
Location/Qualifiers
1. .941
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:6336305"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_130"
/notes="Organ: otcyats; Vector: pCMV-SPORT6.1; Site:1:
EcorRV; Site:2: NotI; Cloned unidirectionally. Primer:
Oligo df. Average insert size 1.95 kb. Constructed by
ResGen, Invitrogen Corp. Note: this is a NIH_MGC Library."

FEATURES
source
Query Match 62.4%; Score 742.6; DB 3; Length 941;
Best Local Similarity 89.9%; Pred. No. 5.9e-171;
Matches 840; Conservative 0; Mismatches 90; Indels 4; Gaps 4;

Qy 225 GCAGATCTTCAACAGAGGACCCAGGAGAAATTCGCCCTCAAAATGCTTCAGGACTGCC 284
Db 1 GCGGATCTTCGACAGAGAACCCAGCAAAAATTCGCCCTAAAGATGCTCCAGGACTGTC 60

Qy 285 CAAGGCCCGCAGGAGGTGAGCTGCATGTCGGGGCTCCAGTCCCGGCACATCGTAGC 344
Db 61 GAAGGCCGCGAGAGGTGGAGCTGCATGTCGGGGCTCCAGTCCCGGCACATCGTAGC 120

Qy 345 GATCGTGGATGTGTACAGAAATCTGTACGAGGAGGAAGTGCCTGCTGATTGTATGGA 404
Db 121 CATCGTGGATGTGTATGAGAACTGTATGTCGGGAGGAAGTGCCTGCTGATTGTATGGA 180

Qy 405 ATGTTTGGACGGTGGAGAACTTTTAGCCGAATCCAGATCGAGGAGACCGAGGCAATTCAC 464
Db 181 GTGTCTCGATGGTGGAGAGCTTTTAGTGAATCCAGGACCGAGGAGACCGAGGCAATTCAC 240

Qy 465 AGAAGAGAGACATCCGAATCATGAAGATCGGTGAGGCCATCCAGTATCTGCATTC 524
Db 241 AGAAGAGAGCGGTGAGAGATCATGAAGATCGGTGAGGCCATCCAGTATCTGCATTC 300

Qy 525 AATCAACATTCGCCATCGGATGTCAAGCCTGAGAATCTTTATACACCTCCAAAAGGCC 584
Db 301 GATCAACATTCGTCACCGGATGTCAAGCCTGAGAACTTTATATCTTCCAAAAGGCC 360

Qy 585 CAAGCCATCTGAAACTACTGACTTTGGCTTTGGCTTTGGCAAGAAACCCAGGCCAATTC 644
Db 361 CAATGCCATTTGAAACTACTGATTTGGCTTTGGCTTTGGCAAGAAACCCAGGCCAATTC 420

Qy 645 TTTCACCACTCTTTGTTATACACCGTACTATGTGCTCCAGAGTGTGGTCCAGAGAA 704
Db 421 TTTCACCACTCTTTGTTATACACCATATCTATGTGCTCCAGAGTGTGGTCCAGAGAA 480

Qy 705 GTATGACAAAGTCTGTGACATGTGCTGCTCCCTGCTCATCATGTATCATCTGCTGTGG 764

Db 481 GTATGACAAAGTCTGTGACATGTGCTGCTCCCTGCTCATCATGTATTTTGTGTGG 540
Qy 765 GTATCCCCCTTCTACTTCCAAACACACCGCCTTGCATCTTCTCCGGCATGAAGACTCGCAT 824
Db 541 GTATCCCCCTTCTATTATCCAAATCACGGCCTTGCATCTTCTCCGGCATGAAGACTCGTAT 600
Qy 825 CGAATGGGCGAGTATGAATTTCCCAACCCAGATCGTTCAGAGTATCAGAGAAAGTGAA 884
Db 601 TCGAATGGGCGAGTATGAATTTCTTAACCCGGAGTGTTCAGAGTATCAGAGAAAGTGAA 660
Qy 885 GATGCTCATTTCCGAATCTGCTGAAAACAGAGCCACCCAGAGAAATGACCATCACAGATT 944
Db 661 GATGCTTATCCGGAATCTGCTGAAAACAGAGCCACCCAGAGAAATGACCATCACAGATT 720
Qy 945 TATGAACACCCCTTGGATCATGCAATCAACAAAGGTCCCTCAAAACCCCATGTCACACAC 1004
Db 721 CATGAACACCCCTTGGATCATGCAATCAACAAAGGTCCCTCAAGACTCCCATGTCACACAC 780
Qy 1005 CCGG-GTTCCTGAGGAGGACAGGAGCGG-TGGGAGGATGTCAAGGA-GGAGATGACCAG 1061
Db 781 CCNGTGTCTCTGAAGGAGGACAGGAGCGGATGGGAGGATGTCAAGGAGGAGATGACCAG 840
Qy 1062 TGCCTT-GGCCACAATGCGCTTTGACTACGAGCAGATCAAGATAAAAAAGATTGAAGATG 1120
Db 841 TGCCTTGGGCCAGATGCGTGTGACTATGAGCAGATCCAGATAAAGAGATAGAGACG 900
Qy 1121 CATCAACCCCTTGTGCTGTAAGAGCGGGAAGAA 1154
Db 901 CATCAACCCCTTGTCTTCTCAAGAGCGGGAAGAA 934

RESULT 6
BG397545 785 bp mRNA linear EST 12-MAR-2001
LOCUS 602439376F1 NIH_MGC_48 Homo sapiens cdna clone IMAGE:4565442 5',
DEFINITION mRNA sequence.
ACCESSION BG397545
VERSION BG397545.1 GI:13290993
KEYWORDS EST.
SOURCE Homo sapiens
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 785)
NIH-MGC http://imgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L18M1282 row: h column: 19
High quality sequence stop: 761.
Location/Qualifiers
1. .785
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/notes="Organ: B-cells; Vector: pOTB7; Site:1: XhoI;
Site:2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >50bp

```

for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 61.9%; Score 737.6; DB 2; Length 785;  
Best Local Similarity 98.3%; Pred. No. 9.6e-170;  
Matches 767; Conservative 0; Mismatches 9; Indels 4; Gaps 2;

Qy 272 TTCAGGAGTGGCCCAAGGCCCGCAGGAGGTGGAGTGCATCGCGGGCTCCAGTGCC 331  
Db |||||  
Qy 2 TTCAGGAGTGGCCCAAGGCCCGCAGGAGGTGGAGTGCATCGCGGGCTCCAGTGCC 61  
Db |||||  
Qy 332 CGCAGCATGTACGGATCGTGATGTACGAGATCTGTACGAGGAGGAGTGCCTGC 391  
Db |||||  
Qy 62 CGCAGCATGTACGGATCGTGATGTACGAGATCTGTACGAGGAGGAGTGCCTGC 121  
Db |||||  
Qy 392 TGATTGTTCATGGAATGTTTGGACGGTGGAGAACTCTTAGCCGAATCCAGGATCGAGGAG 451  
Db |||||  
Qy 122 TGATTGTTCATGGAATGTTTGGACGGTGGAGAACTCTTAGCCGAATCCAGGATCGAGGAG 181  
Db |||||  
Qy 452 ACCAGGATTCACAGAAAGAGAGATCCGAAATCATGAAGAGCATCGTGAGGCCATCC 511  
Db |||||  
Qy 182 ACCAGGATTCACAGAAAGAGAGATCCGAAATCATGAAGAGCATCGTGAGGCCATCC 241  
Db |||||  
Qy 512 AGTATCTGCATTCATCAACATTCGCCATCGGATGTCAGCCTGAGAACTCTTTATACA 571  
Db |||||  
Qy 242 AGTATCTGCATTCATCAACATTCGCCATCGGATGTCAGCCTGAGAACTCTTTATACA 301  
Db |||||  
Qy 572 CCTCCAAAGGCCCAAGCCATCTCGAACTCACTGACTTTGGCTTTGCCAAGAAACCA 631  
Db |||||  
Qy 302 CCTCCAAAGGCCCAAGCCATCTCGAACTCACTGACTTTGGCTTTGCCAAGAAACCA 361  
Db |||||  
Qy 632 CCAGCCCAACTCTTTGACCACTCTTGTATATACACCGTACTATGTGGCTCCAGAAATGC 691  
Db |||||  
Qy 362 CCAGCCCAACTCTTTGACCACTCTTGTATATACACCGTACTATGTGGCTCCAGAAATGC 421  
Db |||||  
Qy 692 TGGTCCAGAGAGTATGACAAAGTCTGTGACATGTCCTGCTGGTGTATCATGATGACA 751  
Db |||||  
Qy 422 TGGTCCAGAGAGTATGACAAAGTCTGTGACATGTCCTGCTGGTGTATCATGATGACA 481  
Db |||||  
Qy 752 TCCTGCTGTGGGTATCCCCCTTCTACTCCAAACACGGCTTGGCATCTCTCCGGGCA 811  
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Qy 482 TCCTGCTGTGGGTATCCCCCTTCTACTCCAAACACGGCTTGGCATCTCTCCGGGCA 541  
Db |||||  
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Db |||||  
Qy 542 TGAAGACTCGCATCCGAAATGGGCCAGTATGAATTTCCAAACCCAGAAATGTCAGAAAT 601  
Db |||||  
Qy 872 CAGAGGAGTGAAGATGCTCATTTGGATCTGTGAAACAGAGCCCAACCCAGAGATGA 931  
Db |||||  
Qy 602 CAGAGGAGTGAAGATGCTCATTTGGATCTGTGAAACAGAGCCCAACCCAGAGATGA 661  
Db |||||  
Qy 932 CCATCACCGAGTTTATGAACCAACCCCTTGGATCATGCAATCAACAAAGGTCCCTCAAAACC 991  
Db |||||  
Qy 662 CCATCACCGAGTTTATGAACCA-CTTTGGATCATGCAATCAACAAAGGTCCCTCAAAACC 720  
Db |||||  
Qy 992 CACTGCAACACAGCGGGTCTTGAAGGAGGACAAAGAGCGGTGGAGGATGTCAAGAGG 1051  
Db |||||  
Qy 721 AATGACA---CCAGCGGTCTCTGAAGGAGGACAAAGGAGCGGTGGAGGATGTCAAGGGG 777  
Db |||||

## RESULT 7

CN431763  
LOCUS 726 bp mRNA linear EST 16-MAY-2004  
DEFINITION 1700600180477 GRN\_PRENU Homo sapiens cDNA 5', mRNA sequence.  
ACCESSION CN431763  
VERSION CN431763.1 GI:47419357  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homniidae; Homo;  
1 (Bases 1 to 726)  
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,  
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,  
Lebkowski, J. and Stanton, L.W.  
Transcriptome characterization elucidates signaling networks that  
control human ES cell growth and differentiation  
Nat. Biotechnol. 22 (6), 707-716 (2004)

15146197

## COMMENT

Contact: Brandenberger R  
Regenerative Medicine  
Geron Corporation  
230 Constitution Drive, Menlo Park, CA 94025, USA  
Tel: 650 473 8558  
Fax: 650 473 7760  
Email: rbrandenberger@geron.com  
Insert Length: 726 Std Error: 0.00.

## FEATURES

source

1..726  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/tissue\_type="embryonic stem cell, retinoic acid and  
mitogen-treated hES cell line H7"  
/clone\_lib="GRN PRENU"  
/note="oligo dT primed, full-length enriched cDNA library  
from hES cell line H7 (p29) maintained in feeder-free  
conditions. Embryoid bodies were generated in the presence  
of all-trans retinoic acid and mitogens."

## ORIGIN

Query Match 60.0%; Score 715; DB 8; Length 726;  
Best Local Similarity 99.3%; Pred. No. 3.3e-164;  
Matches 718; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 294 CAGGAGGTGGAGCTGCATCTGGCGGCTCCAGTCCCGCACATCGTACGGATCGTGGG 353  
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Qy 354 TGTGTACGAGAACTGTGTACGAGGAGGAAGTCCCTGTGATTGTTCATGAAATGTTTGGG 413  
Db |||||  
Qy 64 TGTGTACGAGAACTGTGTACGAGGAGGAAGTCCCTGTGATTGTTCATGAAATGTTTGGG 123  
Db |||||  
Qy 414 CGGTGGAGAACTCTTTAGCCGAATGGGGATCGAGGAGACCGGGATTCACAGAAAGAGA 473  
Db |||||  
Qy 124 CGGTGGAGAACTCTTTAGCCGAATGGGGATCGAGGAGACCGGGATTCACAGAAAGAGA 183  
Db |||||  
Qy 474 AGCATCCGAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCAATCAACAT 533  
Db |||||  
Qy 184 AGCATCCGAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCAATCAACAT 243  
Db |||||  
Qy 534 TGCCCATCGGAGTGTCAAGCTGAGAAATCTTTATACCTCCAAAGGCCCAACGCCAT 593  
Db |||||  
Qy 244 TGCCCATCGGAGTGTCAAGCTGAGAAATCTTTATACCTCCAAAGGCCCAACGCCAT 303  
Db |||||  
Qy 594 CTTGAACTCACTGACTTTGGCTTTGCCAAGGAAACCCAGCCCAACAACTCTTTGACCAC 653  
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Qy 304 CTTGAACTCACTGACTTTGGCTTTGCCAAGGAAACCCAGCCCAACAACTCTTTGACCAC 363  
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Qy 654 TCCTTGTATACACCTGACTATGTGGCTCCAGAAAGTGTGGTCCAGAGAAAGTATGACAA 713  
Db |||||  
Qy 364 TCCTTGTATACACCTGACTATGTGGCTCCAGAAAGTGTGGTCCAGAGAAAGTATGACAA 423  
Db |||||  
Qy 714 GTCTGTGACATGTGTCTCTGGTGTATCATGATGATCATCTCTGTGTGGGTATCCCC 773  
Db |||||  
Qy 424 GTCTGTGACATGTGTCTCTGGTGTATCATGATGATCATCTCTGTGTGGGTATCCCC 483  
Db |||||  
Qy 774 CTTTACTCCAAACCGGCTTGCCTATCTCTCGGGCATGAAGACTCGCATCCGAATGGG 833  
Db |||||  
Qy 484 CTTTACTCCAAACCGGCTTGCCTATCTCTCGGGCATGAAGACTCGCATCCGAATGGG 543  
Db |||||

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QY      834 CCAGTATGAATTTCCCAACCCAGAAATGGTCAGAAAGTATCAGAGAAAGTGAAGATGCTCAT 893
Db      544 CCAGTATGAATTTCCCAACCCAGAAATGGTCAGAAAGTATCAGAGAAAGTGAAGATGCTCAT 603
QY      894 TCGGAATCTGCTGAAACAGAGCCACCCAGAGAAATGACCATACCCAGTTTATGAACCA 953
Db      604 TCGGAATCTGCTGAAACAGAGCCACCCAGAGAAATGACCATACCCAGTTTATGAACCA 663
QY      954 CCCTTGGATCATGCAATCAACAAAGGTCCTTCAAAACCCCACTGCACACCCGCGGTCT 1013
Db      664 CCCTTGGATCATGCAATCAACAAAGGTCCTTCAAAACCCCACTGCACACCCGCGGTCT 723
QY      1014 GAA 1016
Db      724 GAA 726

RESULT 8
DR423458
LOCUS   DR423458
DEFINITION DR423458 710 bp mRNA linear EST 29-JUN-2005
          nav26d01.y1 Human pterygium. Unnormalized (nav) Homo sapiens cDNA
          clone nav26d01 5', mRNA sequence.
ACCESSION DR423458
VERSION   DR423458.1 GI:68325474
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
REFERENCE 1 (bases 1 to 710)
AUTHORS   Wistow,G., Jaworski,C., Aryankalayil-John,M., Rowsey,J.J., Cox,C.,
          Reid,T., Dushku,N. and Carper, D.
TITLE     NEIBank analysis of Human pterygium
JOURNAL   Unpublished (2005)
COMMENT   Contact: Wistow G
          Section on Molecular Structure and Function
          National Eye Institute
          6/331, NIH, Bethesda, MD 20892-2740, USA
          Tel: 301 402 3452
          Fax: 301 496 0078
          Email: graeme@helix.nih.gov
          Plate: 26 row: d column: 01
          Seq primer: Universal M13 Reverse.
          Location/Qualifiers
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               /mol_type="mRNA"
               /db_xref="taxon:9606"
               /clone="nav26d01"
               /tissue_type="Pterygium"
               /dev_stage="Adult"
               /lab_host="EMDH108"
               /clone.lib="Human pterygium. Unnormalized (nav)"
               /note="Organ: Eye; Vector: pCMVSPORT6; RNA was extracted
               from 9 pooled human pterygia. A directionally cloned cDNA
               library in the pCMVSPORT6 vector (Invitrogen) was
               constructed at Bioserve Biotechnology (Laurel MD)
               essentially following the protocols of the SuperScript
               Plasmid System, full details of which are contained in the
               manufacturer's Instruction manual
               (http://www.lifetech.com/). First strand synthesis was
               carried out using a Not I primer-adaptor
               [5'-pGATGATCTAGTCGAGCGCGGCCCTTT15-3']. cDNA was
               cloned in Not I/Sal I sites. EST analysis was performed at
               the NIH Intramural Sequencing Center (NISC). Analyzed data
               available through http://neibank.nei.nih.gov."

FEATURES
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               /dev_stage="Adult"
               /lab_host="EMDH108"
               /clone.lib="Human pterygium. Unnormalized (nav)"
               /note="Organ: Eye; Vector: pCMVSPORT6; RNA was extracted
               from 9 pooled human pterygia. A directionally cloned cDNA
               library in the pCMVSPORT6 vector (Invitrogen) was
               constructed at Bioserve Biotechnology (Laurel MD)
               essentially following the protocols of the SuperScript
               Plasmid System, full details of which are contained in the
               manufacturer's Instruction manual
               (http://www.lifetech.com/). First strand synthesis was
               carried out using a Not I primer-adaptor
               [5'-pGATGATCTAGTCGAGCGCGGCCCTTT15-3']. cDNA was
               cloned in Not I/Sal I sites. EST analysis was performed at
               the NIH Intramural Sequencing Center (NISC). Analyzed data
               available through http://neibank.nei.nih.gov."

ORIGIN
Query Match 59.6%; Score 710; DB 10; Length 710;
Best Local Similarity 100.0%; Pred. No. 5.5e-163;
Matches 710; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      48  GCCGAGCCCCCCCCACCCCTGCTCCGCGCACCCCCCGGCGCAGCGCGCGCGCCCC 107
Db      1  GCCGAGCCCCCCCCACCCCTGCTCCGCGCACCCCCCGGCGCAGCGCGCGCGCCCC 60
QY      108  GCAGCAGTTTCCCGCAGTTCCACGTCGAAGTCCGGCCTGCGAGTCAAGAAGAACGCCATCAT 167
Db      61  GCAGCAGTTTCCCGCAGTTCCACGTCGAAGTCCGGCCTGCGAGTCAAGAAGAACGCCATCAT 120
QY      168  CGATGACTACAAGGTCAACAGCCAGGTCCTTGGGGCTGGGCATCAACGGGCAAAATTTTGCA 227
Db      121  CGATGACTACAAGGTCAACAGCCAGGTCCTTGGGGCTGGGCATCAACGGGCAAAATTTTGCA 180
QY      228  GATCTTCACAGAGGACCCAGAGAAATTCGCCCTCMAAATGCTTCAGGACTGCCCAA 287
Db      181  GATCTTCACAGAGGACCCAGAGAAATTCGCCCTCMAAATGCTTCAGGACTGCCCAA 240
QY      288  GGCCCGCAGGGAGGTGGAGTGCATCTGGGGGCTCCCAAGTCCCGCACATCGTACGGAT 347
Db      241  GGCCCGCAGGGAGGTGGAGTGCATCTGGGGGCTCCCAAGTCCCGCACATCGTACGGAT 300
QY      348  CGTGGATGTGACGAGAAATCTGTACGAGAGGAGGAAGTGCCTGCTGATTTGATGGAATG 407
Db      301  CGTGGATGTGACGAGAAATCTGTACGAGAGGAGGAAGTGCCTGCTGATTTGATGGAATG 360
QY      408  TTTGGACGTTGGAGAACTCTTTAGCCGAATCCAGGATCGAGGAGACGAGCATTCACAGA 467
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QY      468  AAGAGAAGCATCCGAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCAAT 527
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QY      588  CGCATCTCTGAAACTCACTGACTTTTGGCTTTGCCAAGGAAACCAACAGCCACAACCTCTTT 647
Db      541  CGCATCTCTGAAACTCACTGACTTTTGGCTTTGCCAAGGAAACCAACAGCCACAACCTCTTT 600
QY      648  GACCACTCTCTTTATACACCGTACTATGTGGTCCAGAAAGTCTGGGTCCAGAGAAGTA 707
Db      601  GACCACTCTCTTTATACACCGTACTATGTGGTCCAGAAAGTCTGGGTCCAGAGAAGTA 660
QY      708  TGACAAAGTCTGTGACATGTGTCCTTGGGTGTCATCATGTACATCTCTGC 757
Db      661  TGACAAAGTCTGTGACATGTGTCCTTGGGTGTCATCATGTACATCTCTGC 710

RESULT 9
CV804995
LOCUS   CV804995
DEFINITION AGENCOURT_36395066 NIH_MGC_280 Homo sapiens cDNA clone
          IMAGE:7501093 5', mRNA sequence.
ACCESSION CV804995
VERSION   CV804995.1 GI:55747961
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
REFERENCE 1 (bases 1 to 756)
AUTHORS   NIH-MGC http://mgi.nci.nih.gov/
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Daniela S. Gerhard, Ph.D.
          Office of Cancer Genomics
          National Cancer Institute / NIH
          Bldg. 31 Rm10A07 Bethesda, MD 20892
          Email: cgabs-r@mail.nih.gov
          Tissue Procurement: Meri Firpo
          cDNA Library Preparation: Express Genomics

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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LIAW15866 row: 9 column: 11  
 High quality sequence stop: 652.  
 Location/Qualifiers  
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 /db\_xref="taxon:9606"  
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 blastocyst inner cell mass"  
 /lab hosts="DH10B"  
 /clone\_lib="NIH MGC 280"  
 /note="Organ: Blastocyst; Vector: pExpress-1; Site 1:  
 EcorV; Site 2: NotI; RNA obtained from pluripotent cell  
 line derived from blastocyst inner cell mass (cell line  
 HSF-6, NIH Registry designation UC06. Positive for OCT4  
 expression by rtPCR, positive for SSEA-3, SSEA-4,  
 Tra-1-81, Tra-1-60 by immunofluorescence. Negative for  
 SSEA-1 by immunofluorescence passage 62. cDNA was primed  
 using oligo-dT primer:  
 5'-pGACTAGTTCTAGATCGCGAGCGCGCC(T)25-3' and cloned into  
 the EcorV/NotI sites of pExpress-1. Size-selection >1.25  
 kb resulted in an average insert size of 1.8 kb. This  
 primary library is non-normalized (normalized primary  
 library is NIH MGC 281) and was constructed by Express  
 Genomics (Frederick, MD). Note: this is a Mammalian Gene  
 Collection library."

## ORIGIN

Query Match 59.6%; Score 710; DB 8; Length 756;  
 Best Local Similarity 100.0%; Pred. No. 5.6e-163;  
 Matches 710; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 482 AAATCATGAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCAATCAACATTGCCCATC 541  
 Db 1 AAATCATGAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCAATCAACATTGCCCATC 60

Qy 542 GGGATGTCAAGCCTGAGAACTCTTTATACACCTCCAAAAGGCCCAAGCCCATCTCGAAAC 601  
 Db 61 GGGATGTCAAGCCTGAGAACTCTTTATACACCTCCAAAAGGCCCAAGCCCATCTCGAAAC 120

Qy 602 TCACTGACTTTGGCTTTGCCAAGAACCCAGCCACCACTCTTTGACCACTCTTGT 661  
 Db 121 TCACTGACTTTGGCTTTGCCAAGAACCCAGCCACCACTCTTTGACCACTCTTGT 180

Qy 662 ATACACGCTACTATGTGGCTCCAGAAGTGTGGTCCAGAGAAGTATGACAAGTCCTGTG 721  
 Db 181 ATACACGCTACTATGTGGCTCCAGAAGTGTGGTCCAGAGAAGTATGACAAGTCCTGTG 240

Qy 722 ACATGTGGTCCCTGGGTGTTCATCATGTACATCTCTGTGTGGGTATCCCCCTTCTACT 781  
 Db 241 ACATGTGGTCCCTGGGTGTTCATCATGTACATCTCTGTGTGGGTATCCCCCTTCTACT 300

Qy 782 CCAACACGGCTTGGCCATCTCTCCGGGCATGAAGACTCGATCCGAATGGCCAGTATG 841  
 Db 301 CCAACACGGCTTGGCCATCTCTCCGGGCATGAAGACTCGATCCGAATGGCCAGTATG 360

Qy 842 AATTTCACACCCAGAAATGTCAGAAATATCAGAGGAAGTGAAGTCTCATTCGGAATC 901  
 Db 361 AATTTCACACCCAGAAATGTCAGAAATATCAGAGGAAGTGAAGTCTCATTCGGAATC 420

Qy 902 TGCTGAAAAAGAGCCCAACCCAGAGAAATGACCATCCAGGTTTATGAACACCCCTTGA 961  
 Db 421 TGCTGAAAAAGAGCCCAACCCAGAGAAATGACCATCCAGGTTTATGAACACCCCTTGA 480

Qy 962 TCATGCAATCAACAAAGGTCCCTCAAAACCCCACTGCAACACCGCGGTCTGAGGAGG 1021  
 Db 481 TCATGCAATCAACAAAGGTCCCTCAAAACCCCACTGCAACACCGCGGTCTGAGGAGG 540

Qy 1022 ACAAGGAGCGGTGGAGATGTCAAGGAGGAGATGACCACTGCTTGGCCACCAATGCGCG 1081  
 Db 541 ACAAGGAGCGGTGGAGATGTCAAGGAGGAGATGACCACTGCTTGGCCACCAATGCGCG 600

Qy 1082 TTGACTACGAGCAGATCAAGATAAAAAAGATTGAAGATGATCAACCCCTCTGCTGCTGA 1141  
 Db 601 TTGACTACGAGCAGATCAAGATAAAAAAGATTGAAGATGATCAACCCCTCTGCTGCTGA 660

Qy 1142 AGAGCGGAGAAAGCTCGGCGCTCGAGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCT 1191  
 Db 661 AGAGCGGAGAAAGCTCGGCGCTCGAGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCT 710

RESULT 10  
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LOCUS BG779875 720 bp mRNA linear EST 15-MAY-2001  
 DEFINITION 602667370F1 NIH\_MGC\_60 Homo sapiens cDNA clone IMAGE:4807072 5',  
 mRNA sequence.

ACCESSION BG779875

VERSION BG779875.1 GI:14050192

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.

1 (bases 1 to 720)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rc@mail.nih.gov

Tissue Procurement: DCTD/DTF

cDNA Library Preparation: CLONTECH Laboratories, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LCM1657 row: 1 column: 17

High quality sequence stop: 719.

## FEATURES

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 /clone\_lib="NIH MGC 60"  
 /note="Organ: prostate; Vector: pDNR-LIB (Clontech);  
 Site 1: SfiI (ggccgctggcc); Site 2: SfiI  
 (ggccattatggcc); Double-stranded cDNA was prepared from  
 cell line RNA. 5' and 3' adaptors were used in cloning as  
 follows: 5' adaptor sequence: 5'-CACGGCCATTATGGC-3' and  
 3' adaptor sequence:  
 5'-ATTCTAGAGCCGAGCGCGCCGACATG-dt(30)BN-3' (where B = A,  
 C, or G and N = A, C, G, or T). Average insert size 1.5  
 kb (range 0.9-4.0 kb). 14/15 colonies contained inserts  
 by PCR. This library was enriched for full-length clones  
 and was constructed by Clontech Laboratories (Palo Alto,  
 CA). Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 57.8%; Score 688; DB 2; Length 720;  
 Best Local Similarity 99.0%; Pred. No. 1.4e-157;  
 Matches 713; Conservative 0; Mismatches 5; Indels 2; Gaps 2;

Qy 343 CGGATCGTGGATGTACGAGATCTGTACGAGGAGGAGTGCCTGCTGTTGTCATG 402  
 Db 1 CGGATCGTGGATGTACGAGATCTGTACGAGGAGGAGTGCCTGCTGTTGTCATG 60



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Qy 403 GAATGTTTGGACGGTGAGAACTCTTTAGCCGAATCCAGGATCGAGGAGCCAGGCAATTC 462
Db 61 GAATGTTTGGACGGTGAGAACTCTTTAGCCGAATCCAGGATCGAGGAGCCAGGCAATTC 120
Qy 463 ACAGAAAGAGAGCANTCCGAAATCATGAAGAGCATCGGTGAGGCCATCCAGTAGTCTGTCAT 522
Db 121 ACAGAAAGAGAGCANTCCGAAATCATGAAGAGCATCGGTGAGGCCATCCAGTAGTCTGTCAT 180
Qy 523 TCAATCAACATTTGCCATCGGGATGTCAAGCCTGAGAAATCTCTTATACACTCCAAAGG 582
Db 181 TCAATCAACATTTGCCATCGGGATGTCAAGCCTGAGAAATCTCTTATACACTCCAAAGG 240
Qy 583 CCMAAGCCATCTGAAACTCACTGACTTTGGCTTTGCCAAGGAAACCCAGGCCAAC 642
Db 241 CCMAAGCCATCTGAAACTCACTGACTTTGGCTTTGCCAAGGAAACCCAGGCCAAC 300
Qy 643 TCTTTGACCACTCTCTGTATATACACCGTACTATGTGGCTCCAGAAAGTGGTGGTCCAGAG 702
Db 301 TCTTTGACCACTCTCTGTATATACACCGTACTATGTGGCTCCAGAAAGTGGTGGTCCAGAG 360
Qy 703 AAGTATGACAAAGTCTCTGATGTGTGCTCCCTGGGTCTCATGTATACATCCTGCTGTGT 762
Db 361 AAGTATGACAAAGTCTCTGATGTGTGCTCCCTGGGTCTCATGTATACATCCTGCTGTGT 420
Qy 763 GGGTATCCCCCTTCTACTCCAACACCGCTTGGCATCTCTCCGGGCATGAAGACTCGC 822
Db 421 GGGTATCCCCCTTCTACTCCAACACCGCTTGGCATCTCTCCGGGCATGAAGACTCGC 480
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Db 481 ATCCGAATGGGCCAGTATGAATTTCCCAACCCAGAATGGTCAGAAAGTATCAGAGGAAGTG 540
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Qy 1001 CCAGCCGGTCTTGAAGGAGACAAAGGCGGTGGGAGGATGTCAAGGAGGAGATGACCA 1060
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DEFINITION LB03014.CR_J23 GC_BGC-30 Bos taurus cDNA clone IMAGE:8137465, mRNA
sequence.
ACCESSION DV928789
VERSION DV928789.1 GI:82985350
KEYWORDS EST.
SOURCE Bos taurus (cattle)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 902)
Moore S., Alexander, L., Brownstein, M., Guan, L., Lobo, S., Meng, Y.,
Tanaguchi, M., Wang, Z., Yu, J., Prange, C., Schreiber, K., Shenmen, C.,
Wagner, L., Bala, M., Barzak, S., Barber, S., Babakiaff, R.,
Beland, J., Chun, E., Del Rio, L., Gibson, S., Hanson, R.,
Kirkpatrick, R., Liu, J., Matsuo, C., Mayo, M., Santos, R.,
Teai, M., Wong, D., Siddiqui, A., Holt, R., Jones, S.J. and Marra, M.A.
Bovine Genome Sequencing Program: Full-length cDNA Sequencing
Unpublished (2005)
Contact: Robert Kirkpatrick
Canada's Michael Smith Genome Sciences Centre
BC Cancer Agency
Suite 100, 570 West 7th Avenue, Vancouver, British Columbia,
Canada, V5Z 4S6
Tel: 1-604-707-5900 x5406
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Fax: 1-604-876-3561  
Email: robertk@bcgsc.ca  
Insert Length: 902 Std Error: 0.00  
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/dev\_stage="6 months old fetus"  
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/clone\_lib="GC BGC-30"  
/notes="Vector: pExpress 1; Site\_1: Blunt (5' end of cDNA);  
Site\_2: NotI (3' end of cDNA)";

## ORIGIN

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Query Match 56.9%; Score 678; DB 10; Length 902;
Best Local Similarity 92.2%; Pred. No. 4.2e-155;
Matches 714; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

Qy 418 GGAGAACTCTTTAGCCGAATCCAGGATCGAGGAGCCAGGCATTCACAGAAAGAGAGCA 477
Db 2 GGAGAACTGTTCAGTCCGAATCCAGGACCAGGAGAGCCAGGCCCTTCACGGAAAGAGAGGCC 61
Qy 478 TCCGAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCTCAATTCATCAACATTGCC 537
Db 62 TCAGAGATCATGAAGAGCATTCGGGAGGCCATCCAGTATTTGCACTCAATCAACATGCC 121
Qy 538 CATCGGGATGTCAAGCCTGAGAAATCTCTTATACACCTCCAAAAGGCCCAACGCCATCCTG 597
Db 122 CATCGGGATGTCAAGCCCGAGAACTTTTATACACCTCCAAAAGGCCCAATGCGCATTTCTC 181
Qy 598 AAATCACTGACTTTTGGCTTTGCCAAGGAAACCCAGCCAGCCACCACTCTTTGACCACTCCT 657
Db 182 AAATCACTGATTTTGGCTTTGCCAAGGAAACCCAGCAGTCCAACTCTCTGACCACTCCT 241
Qy 658 TGTATACACCGTACTATGTGGCTCCAGAAAGTCTGGGTCCAGAGAGTATGACAGTCC 717
Db 242 TGTACAGCCATCTACGTGGCTCCAGAGGTCTGGGCCAGAGAGTACGACNAAGTCC 301
Qy 718 TGTGACATGTGTCCTGGGTCTCATGTATCATCTCTGCTGTGGGTATCCCCCTTC 777
Db 302 TGTGACATGTGTCCTGGGTGTCTATGTATCATCTCTGCTGTGGGTATCCCCCTTC 361
Qy 778 TACTCCAAACACCGCTTGGCATCTCTCGGGCATGAAGACTCGCATCCGAATGGGCGCAG 837
Db 362 TATTCCAAACCATGGCTTGGCATCTCTCGGGCATGAAGACTCGCATCCGAATGGGCGCAG 421
Qy 838 TATGAATTTTCCCAACCCAGAAATGGTCAGAAAGTATCAGAGGAAGTGAAGATGCTCATTCGG 897
Db 422 TATGAGTTTCCCAACCCAGAAATGGTCAGAAAGTATCAGAGGAAGTGAAGATGCTCATCCGG 481
Qy 898 AATCTGCTGAAACACAGAGCCACCCAGAGNATGACCATCACCAGTTTATGAACCCCT 957
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Qy 958 TGGATCATGCAATCAACAAAGGTCCCTCAAAACCCACTGCACACCCAGCCGGGTCTCTGAAG 1017
Db 542 TGGATCATGCAATCGAAGAGTCCCTCAAAACCCACTGCACACCCAGCCGGGTCTCTGAAG 601
Qy 1018 GAGGACAAAGGAGCGGTGGGAGGATGTCAAGGAGAGATGACCAAGTGTGCTTTGGCCACAATG 1077
Db 602 GAGGACAAAGGAGAGGTGGGAGGACGTCAAGGAGGAGATGACCAAGTGTGCTTTGGCCACATG 661
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QY	1138	CTGAAGAGCGCGAAGAAAGCTCGGGCCCTGTGAGGCTGCGGCTGTGGGCCACTGA	1191
Db	722	CTGAAGAGCGCGAAGAAAGCGCGGGCCCTGTGAGGCGCGGCTGTGCTCACTGA	775
RESULT 12			
AY410231			
LOCUS			
DEFINITION	AY410231	Mus musculus MAPKAPK2 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.	
ACCESSION	AY410231		
VERSION	AY410231.1	GI:39766199	
KEYWORDS	GSS.		
SOURCE	Mus musculus	(house mouse)	
ORGANISM	Mus musculus		
REFERENCE			
AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.		
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios		
JOURNAL	Science	302 (5652), 1960-1963 (2003)	
PUBMED	14671302		
REFERENCE	2	(bases 1 to 780)	
AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.		
TITLE	Direct Submission		
JOURNAL	Submitted (16-NOV-2003)	Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA	
COMMENT		This sequence was made by sequencing genomic exons and ordering them based on alignment.	
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ORIGIN			
Query Match	55.7%	Score 663.2; DB 14; Length 780;	
Best Local Similarity	90.6%	Pred. No. 1.7e-151;	
Matches 707; Conservative	0; Mismatches 73; Indels 0; Gaps 0;		
QY	268	ATGCTTCAGGACTGCCCCAAGGCCGCGAGGAGGTGGAGCTGCACCTGGCGGGCTCCCG 327	
Db	1	ATGCTCCAGACTGTCCGAAGGCGCGAGAGGTGGAGCTGCACCTGGAGGGCTCCCG 60	
QY	328	TGCCCGGCACATCGTACGGATCGTGGATGTGTACAGAAATCTGTACGACGAGGAGGAAGTGC 387	
Db	61	TGCCCACACATTGTGCACATCGTGGATGTCTATGAGAACTGTATGCGCGGAGGAAGTGC 120	
QY	388	CTGCTGATTGTCATGGAAATGTTTGGACGGTGGAGAACTCTTTAGCCGAATCCAGGATCGA 447	
Db	121	CTGCTGATTGTCATGGAGTGTCTCGATGTGTGGAGAGCTCTTTAGTCCGAATCCAGGACCGA 180	
QY	448	GGAGACGAGCATTTACAGAAAGAGAGCATCCGAATCATGAAGAGCATCGGTGAGGCC 507	
Db	181	GGAGACGAGCATTTACAGAAAGAGAGGCGTCAGAGATCATGAAGAGCATCGCGGAGGCC 240	
QY	508	ATCCAGTATCTGCATTCAATCAACATTGGCCATCGGGATGTCGAAGCTGAGAATCTCTTA 567	
Db	241	ATCCAGTACCTGCATCGATCAACATTGCTCACCGGATGTCGAAGCTGAGAATCTCTTA 300	
QY	568	TACACTCCAAAAGGCCCAACGCGCATCTCGAAACTCACTGACTTTGCTTGGTTCACAGGAA 627	



|||||TACACCGTACTATGTGGCTCCAGAGTCTGGGTCCAGAGAGTATGACAAAGTCTCTGGA 539  
Qy 723 CATGTGTTCCCGTGGTGTCTATCATGTATCATCTCTGTGTGGTATCCCGCTTCTACT 781  
Db 540 CATGTGTTCCCGTGGTGTCTATCATGTATCATCTCTGTGTGGTAT-CCCGCTTCTACT 598  
Qy 782 CCAACACCGCTTCCCGTGGTGTCTCTCCGAGCATGAAGACTCGC-ATCCGAAATGGCCAG 837  
Db 599 CCAACACAGGCTTG-CATCTCTCCGCGCTTGACAGACTGGCATCTGATGGGACAG 657  
Qy 838 TATGAATTTCCCAACCCAGAGTGTGTCAGAGTATCAGAGGAGTGAAGATCTCATTCGG 897  
Db 658 TATGACTTTCCCAACCCAGAGTGTGTCAGAGTATCAGAGGAGTGAAGATCTCATACGG 717  
Qy 898 AA-TCTGCTGAAGACAGCCACCCAGAGATGACCATCAGGAGTTTATGAACACCC 956  
Db 718 AATTCTGCTGAAGACAGGAGCCACCCAGAGATGACCATCAGGAGTTTATGAACACCC 777  
Qy 957 TTGGATCATGCAATCAACAAAGGTCCTTCAAAACCCACTGCACACCCAGCGGTCTCGAA 1016  
Db 778 TGGGATCTGGA---TCACAAAGTCTTCAAAACCCATGGGACACCAAGCGGCTGACG 834  
Qy 1017 GGAGACAAAGAGCGGTGGGAGGATGTCAAGGAGGAGATGACCAAG 1061  
Db 835 GAGGCCACAGCAGCGGGCGGAAGAGATGCACAGGACGGAGATAG 879

RESULT 15  
BU609266  
LOCUS  
DEFINITION  
UI-M-FRO-cap-j-12-0-UI.r1 NIH BMAP\_FRO Mus musculus cDNA clone  
IMAGE:6415595 5', mRNA sequence.  
ACCESSION  
BU609266  
VERSION  
BU609266.1 GI:23275481  
KEYWORDS  
EST.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 776)  
NIH-MGC http://mgi.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: Dr. Jim Lin, University of Iowa  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
This clone was contributed by the Brain Molecular Anatomy Project  
(BMAP)

Seq primer: pyx-5.  
Location/Qualifiers  
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/organism="Mus musculus"  
/mol\_type="mRNA"  
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/db\_xref="taxon:10090"  
/clone="IMAGE:6415595"  
/tissue\_type="whole brain"  
/dev\_stage="embryo 13.5,14.5,16.5,17.5dpc"  
/lab\_host="DH10B (TI phage resistant)"  
/clone\_lib="NIH BMAP\_FRO"  
/note="Organ: Brain; Vector: pyx- Asc; Site 1: EcoR I;  
Site 2: Not I; The library was constructed according  
Bonaldi, Lennon and Soares, Genome Research, 6:791-806,  
1996. Denatured RNA was size fractionated on a 1% agarose  
gel. First strand cDNA synthesis was primed with oligo-dr

primer containing a Not I site. Double strand cDNA was  
size selected according to mRNA size fraction, ligated  
with EcoR I adaptor, digested with NotI and then cloned  
directionally into pyX-Asc vector. The library tag  
sequence located between the Not I site and the polyA tail  
is AGCGAGACAG. This library was created for the University  
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the  
Developing Mouse Nervous System', supported by National  
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,  
program coordinator."

## ORIGIN

Query Match 54.8%; Score 652.2; DB 3; Length 776;  
Best Local Similarity 91.4%; Pred. No. 8.7e-149;  
Matches 701; Conservative 0; Mismatches 65; Indels 1; Gaps 1;  
Qy 374 CAGGAGGAAGTGCCTGCTGATGTCATGGAATGTTTGA- CGGTGGAGAACTCTTTAGC 432  
Db 9 CNGGGAGGAAGTGCCTGCTGATGTCATGGAAGTCTCGATNGGTGGAGAGCTCTTTAGT 68  
Qy 433 CGAATCCAGGATCGAGGAGACCGGCAATTCACAGAAAGAGAGCATCCGAAATCATGAAG 492  
Db 69 CGAATCCAGGACCGAGGAGACCGGCAATTCACAGAAAGAGAGCGGTGAGAGATCATGAAG 128  
Qy 493 AGCATCGGTGAGGCAATCCAGTATCTGATTTCAATCAACATTTGCCCATCGGGATGTCAAG 552  
Db 129 AGCATCGGAGGCAATCCAGTATCTGCTCAATCAACATTTGCCCATCGGGATGTCAAG 188  
Qy 553 CTTGAGAATCTTTATACACTTCAAAAGGCCAAACGCCATCTCTGAACTCAGTCTTT 612  
Db 189 CTTGAGAATCTTTATATATCTTCCAAAGGCCAAATGCCATTTTGAAACTCAGTATTT 248  
Qy 613 GGCTTTCCCAAGGAACCCAGGACCAACTCTTTGACCACTCTCTGTTATACACCGTAC 672  
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Qy 973 ACAAAGTCTCTCAAAACCCCACTGCACACAGCGGGTCTCTGAAGGAGGACCAAGGAGCGG 1032  
Db 609 ACAAAGTCTCTCAAAACCCCACTGCACACAGCGGGTCTCTGAAGGAGGACCAAGGAGCGG 668  
Qy 1033 TGGGAGGATCTCAAGGAGGAGATGACCAAGTGCCTTGGCCCAATTCGCGGTGACTACGAG 1092  
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Qy 1093 CAGATCAAGATAAAAGATTTGAAGATGTCATCAACCTCTGCTGCT 1139  
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Search completed: June 19, 2006, 18:05:58  
Job time : 6438 secs

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2006, 15:50:24 ; Search time 7102 Seconds  
(without alignments)  
10723.934 Million cell updates/sec

Title: US-10-469-221-1  
Perfect score: 1191  
Sequence: 1 tccaggccagagccgcg.....ctggcctcgccactga 1191

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: gb\_env.\*  
2: gb\_pat.\*  
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6: gb\_ro.\*  
7: gb\_sts.\*  
8: gb\_sy.\*  
9: gb\_un.\*  
10: gb\_vi.\*  
11: gb\_ov.\*  
12: gb\_htg.\*  
13: gb\_in.\*  
14: gb\_om.\*  
15: gb\_ba.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1191	100.0	2974	5	BC052584 Homo sapi
2	1189.4	99.9	1690	5	BC036060 Homo sapi
3	1181.4	99.2	1336	2	AR380852 Sequence
4	1181.4	99.2	1336	5	X75346 H. sapiens m
5	1048.4	88.0	2258	2	AR270852 Sequence
6	1048.4	88.0	2258	2	AX335055 Sequence
7	1048.4	88.0	2258	5	U12779 Human MAP k
8	982	82.5	1305	2	DD182194 Methods a
9	967.4	81.2	1065	8	AV335730 Synthetic
10	930	78.1	2909	6	AY197741 Rattus no
11	928.4	78.0	2586	6	BC063064 Mus muscu
12	928.4	77.8	2862	6	BC062048 Rattus no
13	926.8	77.0	2604	6	BC052206 Mus muscu
14	923	77.5	1247	6	X76850 M. musculus
15	836.4	70.2	1168	2	CS214061 Sequence
16	836.4	70.2	1168	6	CLMAPKAP
17	857.6	55.2	3285	11	BC054572 Danio rer
18	656.6	55.1	768	14	X75345 O. cuniculus

19	656.2	55.1	2786	11	CR761979
20	637.6	53.5	2503	11	BC084300 Xenopus l
21	637.6	53.5	2977	11	BC070986 Xenopus l
22	563.6	47.3	2654	14	BC103321 Bos tauru
23	555.8	46.7	1149	8	AY335561 Synthetic
24	555.8	46.7	1149	8	AY892450 Synthetic
25	555.8	46.7	1149	8	AY892451 Synthetic
26	555.8	46.7	1149	8	BT008118 Synthetic
27	555.8	46.7	1298	5	HSU43784 Human mitog
28	555.8	46.7	2481	2	AR270525 Sequence
29	555.8	46.7	2481	5	HSU09578 Homo sapien
30	555.8	46.7	2494	5	BC007591 Homo sapi
31	555.8	46.7	2519	5	BC001662 Homo sapi
32	555.8	46.7	2523	5	BC010407 Homo sapi
33	546.6	45.9	2634	6	BC081974 Rattus no
34	544.6	45.7	2856	6	BC031467 Mus muscu
35	533.8	44.8	2484	2	CQ716382 Sequence
36	528	44.3	1333	2	AR145880 Sequence
37	476	40.0	1952	6	BC024559 Mus muscu
38	448.2	37.6	1982	13	DMU20757 Drosophila
39	448.2	37.6	2000	2	CQ577905 Sequence
40	448.2	37.6	2025	2	CQ601278 Sequence
41	404	33.9	2049	13	D82877 Hemicecentrot
42	391.6	32.9	1544	13	DQ307182 Glossina
43	366	30.7	600	2	CS217703 Sequence
44	269.2	22.6	195485	5	AL591846 Human DNA
45	238.4	20.0	502	2	CQ922313 Sequence

## ALIGNMENTS

RESULT 1	BC052584	2974 bp	mRNA	linear	PRI 30-JUN-2004
LOCUS	Homo sapiens mitogen-activated protein kinase-activated protein kinase 2, transcript variant 2, mRNA (cdna clone MGC:59706 IMAGE:6267183), complete cds.				
DEFINITION	BC052584				
ACCESSION	BC052584.1	GI:30851682			
VERSION	MGC.				
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 2974)				
AUTHORS	Krausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shennen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,I.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.J., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Hulyk,S.W., Fahey,J., Helton,E., Kettman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butlerfield,Y.S., Krzywinski,M.I., Skalska,U., Smalhus,D.E., Scherch,A., Schein,J.E., Jones,S.J. and Marra,M.A.				
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)				
PUBMED	12477932				
REFERENCE	2 (bases 1 to 2974)				
AUTHORS	Krausberg,R.				
TITLE	Direct Submission				
JOURNAL	Submitted (16-MAY-2003) National Institutes of Health, Mammalian				





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Qy      781  TCCAAACACAGCGCTTGCCTCTCTCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT  840
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RESULT 3
LOCUS   AR380852 1336 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1397 from patent US 6607879.
ACCESSION AR380852
VERSION AR380852.1 GI:40088486
KEYWORDS
SOURCE  Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 1336)
AUTHORS Cocks,B.G., Stuart,S.G. and Seilhamer,J.J.
TITLE Compositions for the detection of blood cell and immunological response gene expression
JOURNAL Patent: US 6607879-A 1397 19-AUG-2003;
Incyte corporation; Palo Alto, CA
FEATURES
source 1..1336
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Query Match 99.2%; Score 1181.4; DB 2; Length 1336;
Best Local Similarity 99.5%; Pred. No. 2.2e-310;
Matches 1185; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy      361  GAGAATCTGTACGACGAGGAGAGTCCCTGCTGCTGATGTCATGAAATGTTTGGACGGTGA  420
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Qy      421  GAACTCTTTAGCCGAATCCAGGATCGAGGAGACAGGCAATTCACAGAAAGAGAAGCATCC  480
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RESULT 4
HSMAPKAP 1336 bp mRNA linear PRI 03-JAN-1994
LOCUS HSMAPKAP
DEFINITION H.sapiens mRNA for MAP kinase activated protein kinase.
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Qy 841 GAATTTCCCAACCCAGCAATGGTCAGAGTATCAGAGAAAGTGAAGATGCTCATTCGGAAT 900
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RESULT 8
LOCUS DD182194 1305 bp DNA linear PAT 19-DEC-2005
DEFINITION Methods and Compositions for Protein Expression and Purification.
ACCESSION DD182194
VERSION DD182194.1 GI:83957055
KEYWORDS JP 2005514025-A/15.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 1305)
AUTHORS Malakhova,O.A., Butt,T.R., Tran,H.T., Malakhov,M.P. and Weeks,S.D.
TITLE Methods and Compositions for Protein Expression and Purification
JOURNAL Patent: JP 2005514025-A 15 19-MAY-2005;
Tauseef Butt,Stephen Weeks,Hiep Tran,Oxana Malakhova, Micheal
Malakhov
COMMENT OS Artificial Sequence
PN JP 2005514025-A/15
PD 19-MAY-2005
PF 07-JAN-2003 JP 2003557532
PR 07-JAN-2002 US 607346449
PI oxana a malakhova,tauseef r butt,hiep t tran,micheal p PI
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Best Local Similarity 100.0%; Pred. No. 4.9e-256;
Matches 982; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 9
AY335730 1065 bp mRNA linear SYN 08-JUN-2005
LOCUS Synthetic construct Homo sapiens mitogen-activated protein
DEFINITION kinase-activated protein kinase 2 (MAPKAPK2) mRNA, partial cds.
ACCESSION AY335730
VERSION AY335730.1 GI:33304098
KEYWORDS FLU_CDNA.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 1065)
AUTHORS Park,J., Hu,Y., Murthy,T.V.S., Vannberg,F., Shen,B., Rolfs,A.,
Hutt,J.E., Cantley,L.C., LaBaer,J., Harlow,E. and Brizuela,L.
TITLE Building a human kinase gene repository: Bioinformatics, molecular
cloning, and functional validation
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 102 (23), 8114-8119 (2005)
PUBMED 15928075
REFERENCE 2 (bases 1 to 1065)
AUTHORS Park,J., Rolfs,A., Hu,Y., Shen,B., Vannberg,F., Moreira,D.,
Kelley,T., Zuo,D., Raphael,J., Baqui,M., Jepsen,D., Harlow,E.,
LaBaer,J. and Brizuela,L.

```

**TITLE**  
JOURNAL

**COMMENT**  
Direct Submission  
Submitted (02-JUL-2003) Biological Chemistry and Molecular  
Pharmacology, Harvard Institute of Proteomics, 320 Charles St.,  
Cambridge, MA 02141-2023, USA  
This CDS clone is a part of a collection of human full-length  
expression clones generated by Harvard Institute of Proteomics.  
Each CDS has been cloned without stop-codon (to allow fusion with  
C-terminal tag). The CDS has been directionally cloned using BD  
In-Fusion(TM) cloning system between the Sali and HindIII sites of  
the pNR-Dual vector. Additional sequences in the clone: 'ACC'  
after Sali site and before 'ATG' to provide kozak consensus  
sequence; 'GG' after last codon and before HindIII site to maintain  
reading frame.

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/clone\_lib="First strand cDNA from placenta and brain"  
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1. .>1065  
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1. .>1065  
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LHSINTAHDRVDPENLLYITABKFNAILKLTDFGFKETTSNLSLTPCVTPYVAVPEV  
LGPEKIDKRVNDSGLVIMYILLGVPFYPHNGLAISPGMKTRIRMGQVFFPNPWS  
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DVKGCLHDKNSDQATWLTLL"

**gene**  
CDS

**ORIGIN**

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Best Local Similarity 97.9%; Pred. No. 4.6e-252;  
Matches 980; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

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DB 14 CCAGGGCCAGAGCCCGCGTGCCTGCGCGCGCGCGCGCGCGCGCGCG 73

QY 110 AGCAGTTCGCGAGTCCAGCTCAAGTCCGCGCTGCAGATCAAGAGAGCCATCATCG 169  
DB 74 AGCAGTTCGCGAGTCCAGCTCAAGTCCGCGCTGCAGATCAAGAGAGCCATCATCG 133

QY 170 ATGACTACAAGGTCACAGCCAGCTCTCGGGCTGGGCATCAACGGCAAGTTTGCAGA 229  
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QY 230 TCTTCAACAGAGACCCAGAGAAATTCGCCCTCAAAATGCTTCAGGACTGCCCAAGG 289  
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QY 290 CCGCAGGAGGTGGAGCTGCACCTGGCGGCGCTCCAGTCCCGCACATCGTACGATCG 349  
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QY 350 TGGATGTGACGAGATCTGTACGAGGAGGAAGTGCCTGCTGATTGTGATGGAATGTT 409  
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QY 410 TGGACGCTGGAGAACTCTTTAGCCGAATCCAGGATCAGAGAGACCAGGCATTCACAGAA 469

DB 374 TGGACGCTGGAGAACTCTTTAGCCGAATCCAGGATCCAGGAGACCAGGCATTCACAGAA 433

QY 470 GAGAGCATCCGAATCATCAAGAGATCGGTGAGGCCATCCAGTATCTGCATTCAATCA 529

DB 434 GAGAGCATCCGAATCATCAAGAGATCGGTGAGGCCATCCAGTATCTGCATTCAATCA 493

QY 530 ACATTGCCCATCCGGATGTCAAGCCTGAGAAATCTCTTATACACTCCAAAAGGCCCAACG 589

DB 494 ACATTGCCCATCCGGATGTCAAGCCTGAGAAATCTCTTATACACTCCAAAAGGCCCAACG 553

QY 590 CCATCTCTGAAACTCACTGACTTTGGCTTTGCCAAGAAACACACAGCCCACTCTTTGA 649

DB 554 CCATCTCTGAAACTCACTGACTTTGGCTTTGCCAAGAAACACACAGCCCACTCTTTGA 613

QY 650 CCATCTCTGTTATATACACCGTACTATGTGGCTCCAGAGTGTGGGTCCAGAGAGTATG 709

DB 614 CCATCTCTGTTATATACACCGTACTATGTGGCTCCAGAGTGTGGGTCCAGAGAGTATG 673

QY 710 ACAAGTCTCTGATGATGTGCTCCCTGGGTGTCATCATGTATACATCTCTGCTGGGTATC 769

DB 674 ACAAGTCTCTGATGATGTGCTCCCTGGGTGTCATCATGTATACATCTCTGCTGGGTATC 733

QY 770 CCCCCTTCTACTCAACACCGCTTGCCTTCCCATCTCTCCGGGCATGAAGACTCCGATCCGAA 829

DB 734 CCCCCTTCTACTCAACACCGCTTGCCTTCCCATCTCTCCGGGCATGAAGACTCCGATCCGAA 793

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QY 890 TCATTCCGAATCTGCTGAAACAGAGCCCAACAGAGTATGATCATCACCAGTATTTATGA 949

DB 854 TCATTCCGAATCTGCTGAAACAGAGCCCAACAGAGTATGATCATCACCAGTATTTATGA 913

QY 950 ACCACCTTGGATCATGCAATCAACAAAGTTCCTCAAAACCCCACTGCACACACGCGGG 1009

DB 914 ACCACCTTGGATCATGCAATCAACAAAGTTCCTCAAAACCCCACTGCACACACGCGGG 973

QY 1010 TCCTGAAGGAGGACAGGAGCGGTGGAGATGTCAGGAG 1050

DB 974 TCCTGAAGGAGGACAGGAGCGGTGGAGATGTCAGGAG 1014

**RESULT 10**  
AY197741  
LOCUS  
DEFINITION  
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Rattus norvegicus mitogen-activated protein kinase-activated  
protein kinase-2 mRNA, complete cds.  
AY197741.1 GI:28629390  
KEYWORDS  
SOURCE  
Rattus norvegicus (Norway rat)  
ORGANISM  
Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Muridae; Muridae; Rattus;  
REFERENCE  
1 (bases 1 to 2909)  
Vician, L.J., Xu, G., Liu, W., Feldman, J.D., Machado, H.B. and  
Herschman, H.R.  
MAPKAP Kinase-2 is a Primary Response Gene Induced by  
Depolarization in PC12 Cells and in Brain  
Unpublished  
2 (bases 1 to 2909)  
Vician, L.J., Xu, G. and Herschman, H.R.  
AUTHORS  
Direct Submission  
Submitted (16-DEC-2002) Biological Chemistry, UCLA, 611 Charles E.  
Young Dr. East, Los Angeles, CA 90095-1570, USA  
LOCATION/Qualifiers  
1. .2909  
/organism="Rattus norvegicus"  
/mol\_type="mRNA"  
/strain="BN"  
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3' UTR  
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302. .1462  
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QY 818 CTCGCATCCGAATGGGCCAGTATGAATTTCCCAACCAAGATGCTCAGAAAGTATCAGAGG 877  
Db 1089 CTCGCATCCGAATGGGCCAGTATGAATTTCCCAACCAAGATGCTCAGAAAGTATCAGAGG 1148  
QY 878 AAGTGAAGATGCTCATTCGGAATCTCTGAAACACAGAGCCCAACCCAGAGAATGACCATCA 937  
Db 1149 AAGTGAAGATGCTCATTCGGAATCTCTGAAACACAGAGCCCAACCCAGAGAATGACCATCA 1208  
QY 938 CCAGTATTAAGAACACCCCTTGATCATGCAATCAACAAAGTCCCTCAAAACCCCACTGC 997  
Db 1209 CAGATTCATGAACCAACCCCTTGATCATGCAATCTCAAGAGGTCCTCAGACTCCACTGC 1268  
QY 998 ACACCAAGCGGGTCTGAAAGGAGGACAAAGAGCGGTGGGAGGATGTCAGAGGAGATGA 1057  
Db 1269 ACACCAAGCGGTCTGAAAGGAGGACAAAGAGGATGTCAGAGGAGATGA 1328  
QY 1058 CCAAGTCCCTTGGCCACAATCGCGTTGACTACAGCAGATCAAGATAAAGAAAGATTGAAG 1117  
Db 1329 CCAAGTCCCTTGGCCACGATCGGTGTCGACTATGAGCAGGTCAAGATAAAGAAAGATAGAG 1388  
QY 1118 ATGCATCCAAACCTCTGCTGCTGAAGAGCGGGAAGAGCTCGGCGCTTGGAGGCTGCGG 1177  
Db 1389 ACGCATCCAAACCTCTGCTTCTCAAGAGGAGGAAGAGCTCGGCGCTTGGAGAGCGCGG 1448  
QY 1178 CTCTGGCCCACTGA 1191  
Db 1449 CCCTTGGCCCACTGA 1462

RESULT 11  
BC063064  
LOCUS  
DEFINITION  
Mus musculus MAP kinase-activated protein kinase 2, mRNA (cdna  
clone MGC:67217 IMAGE:5687007), complete cds.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
BC063064.1 GI:38969982  
Mus musculus (house mouse)  
Mus musculus  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridea; Muridae; Murinae; Mus.  
1 (bases 1 to 2586)  
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,  
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,  
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,  
Hopkins, R.F., Jordan, H., Moore, F., Max, S.I., Wang, J., Hsieh, F.,  
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,  
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,  
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,  
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,  
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,  
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,  
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,  
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,  
Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,  
Shanecz, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,  
Bouffard, G., Blakesley, R.W., Touchman, J.W., Green, E.D.,  
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,  
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.E.,  
Schnerk, A., Schein, J.E., Jones, S.J., Marra, M.A.  
Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
12477932  
2 (bases 1 to 2586)  
Strausberg, R.  
Direct Submission















Db 961 GCCGTGAGGCCGAGCCCTTGCCCACTGA 990

Search completed: June 19, 2006, 18:02:38  
Job time : 7105 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 19, 2006, 08:51:36 ; Search time 298 Seconds  
(without alignments)  
1229.215 Million cell updates/sec

Title: US-10-469-221-2

Perfect score: 2106

Sequence: 1 SQGSPVPFPAPAPPQP.....PLLLKRRKKARALEAALAH 396

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 7.2.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2106	100.0	400	1	MAPK2 HUMAN
2	2106	100.0	400	2	Q5SY41 homo sapien
3	1931	91.7	386	1	MAPK2 MOUSE
4	1931	91.7	386	2	Q3U2P8 mus musculus
5	1930	91.6	386	2	Q80ZF4 rattus norv
6	1882	89.4	370	2	Q5SY30 homo sapien
7	1709	81.1	329	1	MAPK2 CRILLO
8	1687	80.1	377	2	Q6IRB4 xenopus lae
9	1661.5	78.9	374	2	Q5XGX7 xenopus lae
10	1645	78.1	382	2	Q7T2F2 brachydanio
11	1536	72.9	330	1	MAPK2_RABIT
12	1468	69.7	340	2	Q4SRA0 TETING
13	1391	66.0	382	1	MAPK3 HUMAN
14	1371	65.1	384	1	MAPK3 RAT
15	1370	65.1	384	1	MAPK3 BOVIN
16	1361	64.6	384	1	MAPK3_MOUSE
17	1344.5	63.8	418	2	Q4RXU6 TETING
18	1340	63.6	416	2	Q4SRA0 TETING
19	1266	60.1	353	2	Q2PQ11 GLOMR
20	1243.5	59.0	350	2	Q25108 HEMPU
21	1211.5	57.5	347	2	Q7PZG1 ANOGA
22	1201	57.0	359	1	MAPK2_DROME
23	1060.5	50.4	391	2	Q61A12 CAEBR
24	1046	49.7	443	2	Q9TZ16 CAEBR
25	1035	49.1	366	2	Q965G5 CAEBR
26	953	45.3	181	2	Q8R3U8 MOUSE
27	796.5	37.8	521	2	Q21360 CAEBR
28	788	37.4	520	2	Q61ZD7 CAEBR
29	740	35.1	495	2	Q6DEV6 XENTR
30	738	35.0	471	2	Q3UV25 MOUSE
31	738	35.0	473	1	MAPK5_MOUSE

RESULT 1

MAPK2\_HUMAN STANDARD; PRT; 400 AA.

AC P49137; Q8IYD6;

DT 01-FEB-1996, integrated into UniProtKB/Swiss-Prot.

DT 01-FEB-1996, sequence version 1.

DT 07-MAR-2006, entry version 52.

DE MAP kinase-activated protein kinase 2 (EC 2.7.1.-) [MAPK-activated protein kinase 2] (MAPKAP kinase 2) (MAPKAPK-2).

DE Name=MAPKAPK2;

GN Homo sapiens (Human).

OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

OC Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE [MRNA].

RX MEDLINE=94235003; PubMed=8179591;

Zu Y.-L., Wu F., Gilchrist A., Ai Y., Labadia M.E., Huang C.K.;

RT "The primary structure of a human MAP kinase activated protein kinase 2";

RT Biochem. Biophys. Res. Commun. 200:1118-1124 (1994).

RN [2]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).

RC TISSUE=Skin, and Testis;

RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickinson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";

RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [3]

RP NUCLEOTIDE SEQUENCE [MRNA] OF 5-400.

RX MEDLINE=94107253; PubMed=8280084;

RA Stokoe D., Caudwell B., Cohen P.T.W., Cohen P.;

RT "The substrate specificity and structure of mitogen-activated protein kinase-2";

RT Biochem. J. 296:843-849 (1993).

RN [4]

## ALIGNMENTS

32 737.5 35.0 363 2 Q7JM88 CAEBL  
33 733 34.8 473 1 MAPK5 HUMAN  
34 730 34.7 471 2 Q6DHN7 BRARE  
35 717 34.0 459 2 Q4RPT6 TETNG  
36 714.5 33.9 346 2 Q65ZB7 CAEBL  
37 655.5 31.1 238 2 Q65ZB6 CAEBL  
38 613 29.1 201 2 Q8T9D6 DROME  
39 566.5 26.9 249 2 Q8QGH1 CHICK  
40 564 26.8 336 2 Q8I117 CAEBL  
41 560.5 26.6 369 2 Q4KLJ9 RAT  
42 543.5 25.8 508 1 CDPK2\_PLAF7  
43 543.5 25.8 512 1 CDPK2\_PLAFK  
44 540 25.6 578 2 Q5SYM5 HUMAN  
45 540 25.6 735 1 KS6A1\_HUMAN

Q7JM88 caenorhabdi  
Q8I1W1 homo sapien  
Q6DHN7 brachydanio  
Q4RPT6 tetraodon n  
Q65ZB7 caenorhabdi  
Q65ZB6 caenorhabdi  
Q8T9D6 drosophila  
Q8QGH1 gallus gall  
Q8I117 caenorhabdi  
Q4KLJ9 rattus norv  
Q8ICR0 plasmodium  
Q15865 plasmodium  
Q5SYM5 homo sapien  
Q15418 homo sapien



Db 5 SQGSPVPFPAPAPPQPTPALPHPPAQQPPPPPPQPFQFHVKSGLQIKKNAIIDDYK 64  
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## RESULT 2

Q5SY41\_HUMAN PRELIMINARY; PRT; 400 AA.  
AC Q5SY41;  
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.  
DT 07-FEB-2006, entry version 11.  
DE Mitogen-activated protein kinase-activated protein kinase 2.  
GN Name=MAPKAPK2; ORFNames=RPL1-343H5.3-001;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP Harrison E.;  
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
CC EMBL: AL591846; CA113544.1; -, Genomic\_DNA.  
DR SMR; Q5SY41; 41-357.  
DR Ensembl; ENSG00000162889; Homo sapiens.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:000166; F:nucleotide binding; IEA.  
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0006458; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR008271; Ser\_Thr\_pkin\_AS.  
DR InterPro; IPR002290; Ser\_Thr\_pkinase.  
DR InterPro; IPR001245; Tyr\_pkinase.  
DR Pfam; PF00069; Pkinase; 1.  
DR SMART; SM00220; S\_PKC; 1.  
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DR PROSITE; PS00108; PROTEIN KINASE ST; 1.  
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KW Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 400 AA; 45568 MW; E4EFPF11CCP288DC CRC64;

Query Match 100.0%; Score 2106; DB 2; Length 400;  
Best Local Similarity 100.0%; Pred. No. 7.1e-115;

Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 365 VDYEQIKIKKIEDASNPILLKRRKKARALEAAALAH 400

RESULT 3  
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ID P49138; Q6P561;  
DT 01-FEB-1996, integrated into UniProtKB/Swiss-Prot.  
DT 04-JAN-2005, sequence version 2.  
DT 07-FEB-2006, entry version 47.  
DE MAP kinase-activated protein kinase 2 (EC 2.7.1.-) (MAPK-activated  
DE protein kinase 2) (MAPKAP kinase 2) (MAPKAPK-2).  
DE Name=Mapkapk2; Synonyms=Rps6kcl;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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OC Muroidae; Muridae; Murinae; Mus.  
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RC TISSUE=Lung;  
RX MEDLINE=94085571; PubMed=8262198; DOI=10.1016/0014-5793(93)81628-D;  
RA Engel K., Plath K., Gaestel M.;  
RT "The MAP kinase-activated protein kinase 2 contains a proline-rich  
RL SH3-binding domain.";  
RL FEBS Lett. 336:143-147(1993).  
RN [2]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RC STRAIN=C57BL/6; TISSUE=Brain;  
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
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RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,





RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,  
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,  
RA Mottaqui-Tabar S., Mulder N., Nakano N., Nakano M., Nakauchi H., Ng P.,  
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,  
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,  
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,  
RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,  
RA Schonbach C., Sekiguchi K., Semple C.A., Sessa L., Sheng Y.,  
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RA Sperling S., Stupka E., Sugiyama K., Sultana R., Takenaka Y., Taki K.,  
RA Tamoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,  
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.B., Yagi K.,  
RA Yananishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,  
RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,  
RA Walestedt C., Tattick J.S., Hume D.A., Kai C., Sasaki K., Tomaru Y.,  
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,  
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,  
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,  
RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,  
RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,  
RA Hayashizaki Y.;  
RT "The transcriptional landscape of the mammalian genome.";  
RL Science 309:1559-1563(2005).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=NOD;  
RX PubMed=16141073; DOI=10.1126/science.1112009;  
RG RIKEN Genome Exploration Research Group, and Genome Science Group  
RT (Genome Network Core Team) and the FANTOM Consortium;  
RT "Antisense Transcription in the Mammalian Transcriptome";  
RL Science 309:1564-1566(2005).  
RN [4]  
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RC STRAIN=NOD;  
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
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RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
RA Balzarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
RA Schriber L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
RA Kanagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
RA Meglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,  
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
RA Verardo R., Wagner L., Walestedt C., Wang Y., Watanabe Y., Wells C.,  
RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
RA Yuan Z., Zavalon M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
RA Birney E., Hayashizaki Y.;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs";  
RL Nature 420:563-573(2002).  
RN [5]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=NOD;  
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
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RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
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RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
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RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,  
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection";  
RL Nature 409:685-690(2001).  
RN [6]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=NOD;  
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
RT prepare full-length cDNA libraries for rapid discovery of new genes";  
RL Genome Res. 10:1617-1630(2000).  
RN [7]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=NOD;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,  
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,  
RA Suni M., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
RT sequencing pipeline with 384 multicapillary sequencer";  
RL Genome Res. 10:1757-1771(2000).  
RN [8]  
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RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,  
RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,  
RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,  
RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,  
RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,  
RA Muramatsu M., Hayashizaki Y.;  
RA Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase families.  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NoDerivs License  
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CC EMBL: AK155171; BAE33092.1; -; mRNA.  
CC MGI: MGI:109298; Mapkapk2.  
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CC GO: GO:0005634; C:nucleus; IDA.  
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CC InterPro: IPR008271; Ser\_thr\_kinase.  
CC InterPro: IPR002290; Ser\_thr\_kinase.  
CC InterPro: IPR001245; Tyr\_kinase.  
CC Pfam: PF00069; Pkinase; I.  
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CC PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
CC ATP-binding; Kinase; Nucleotide-binding;  
CC Serine/threonine-protein kinase; Transferase.  
CC SEQUENCE 386 AA; 44050 MW; ED7827641A826BF3 CRC64;

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RESULT 5
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DT 07-FEB-2006, entry version 23.
DE Mitogen-activated protein kinase-activated protein kinase-2
DE (EC 2.7.1.-) (MAP kinase-activated protein kinase 2).
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RA Vician L.J., Xu G., Liu W., Feldman J.D., Machado H.B.,
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[2]
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RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Sapletton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
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RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
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RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[3]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Prostate;
RC Strausberg R.;
RA Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
RL -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -----
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CC -----
DR EMBL; AY197741; AAC34665.1; -; mRNA.
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DR HSSP; P49137; 1NY3.
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DR GO; GO:0000166; F:nucleotide binding; IEA.
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DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Nucleotide-Binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 386 AA; 44036 MW; 66E827641A827502 CRC64;

Query Match          91.6%; Score 1930; DB 2; Length 386;
Best Local Similarity 92.7%; Pred. No. 1.3e-104;
Matches 367; Conservative 8; Mismatches 7; Indels 14; Gaps 2;

QY 1 SQGSPVPVPAPAPPQPPTPALPHPPAQPQPFPQFHVKSLQIKKNAIIDYK 60
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 Db 241 QRMWTFMFNHPWIMQSTKVPQTPPLHTSRVLKEDKERWEDVKEEMTSALATMRVDYEQIK 300  
 Qy 368 IKKIEDASNPILLKRRKKARALEAALAH 396  
 Db 301 IKKIEDASNPILLKRRKKARALEAALAH 329

## RESULT 8

Q61RB4\_XENLA PRELIMINARY; PRT; 377 AA.

Q61RB4;

DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.

DT 07-FEB-2006, sequence version 1.

DE MGC78852 protein.

GN Name=MGC78852;

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;

OC Xenopodinae; Xenopus; Xenopus.

OX NCBI\_TaxID=8355;

RNA [1]

NUCLEOTIDE SEQUENCE.

RT TSSUS=Embryo;

RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.I., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,

RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RNA [2]

NUCLEOTIDE SEQUENCE.

RT TSSUS=Embryo;

RC MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;

RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,

RA Richardson P.;

RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus

initiative."

RL Dev. Dyn. 225:384-391(2002).

RNA [3]

NUCLEOTIDE SEQUENCE.

RT TSSUS=Embryo;

RA Klein S., Strausberg R.;

RL Submitted (May-2004) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.

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CC -----

DR EMBL; BC070986; AH70986.1; -; mRNA.

DR HSP; Q63450; 1A06.

DR SMR; Q61RB4; 21-337.

DR GO; GO:0005524; F-ATP binding; IEA.

DR GO; GO:0001666; F-nucleotide binding; IEA.

DR GO; GO:0004674; F-protein serine/threonine kinase activity; IEA.

DR GO; GO:0016740; F-transferase activity; IEA.

DR GO; GO:0006468; P-protein amino acid phosphorylation; IEA.

DR InterPro; IPR000719; Prot kinase.

DR InterPro; IPR002290; Ser Thr\_pkin AS.

DR InterPro; IPR001245; Tyr\_pkinase.

DR Pfam; PF00069; Pkinase; 1.

DR ProDom; PD000001; Prot\_kinase; 1.

DR SMART; SM00220; S\_TKc; 1.

DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN 1.

DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.

DR PROSITE; PS00108; PROTEIN\_KINASE ST; 1.

KW ATP-binding; Kinase; Nucleotide-binding;

KW Serine/threonine-protein kinase; Transferase.

SQ SEQUENCE 377 AA; 43551 MW; B488B7AB45ECA81 CRC64;

Query Match 80.1%; Score 1687; DB 2; Length 377;

Best Local Similarity 84.3%; Pred. No. 1.9e-90;

Matches 321; Conservative 19; Mismatches 27; Indels 14; Gaps 2;

Qy 5 SPVPPFPAPAPPQPTPALPHPPAPQPPPPPPQPFQFHVKSLQIKNAIIDYKVTSQ 64

Db 3 NPGIPF-----PNLPALNQTVPQ-----QQQQQQQLKSLQIKNAITDDYKVTNQ 48

Qy 65 VLGLGINKVLQIIFNKRTQKFKALKMLQDCPKARREVELHWRASQCPHIYDVIDVYENLY 124

Db 49 VLGLGINKVRLVLEIFSKRTGKFKALKMLQDCPKARREVDLHWRASQCAHIYKIDVYENLY 108

Qy 125 AGKCLLIIVMECLDGGELFSRIQDRGQAFTEREASEIMKSIGEAIOYLHSINIAHRDVK 184

Db 109 QSRKCLLIIMECLDGGELFSRIQDRGQAFTEREASEIMKSIGEAIOYLHSINIAHRDVK 168

Qy 185 PENLLYTSKRPNAILKLTDFGFAKETTSNLSLTTPCYTPYVAPEVLGPKEKDKSCDMWS 244

Db 169 PENLLYTSKRPNYVLKLTDFGFAKETTTTHNSLATPCYTPYVAPEVLGPKEKDKSCDMWS 228

Qy 245 LGVIMVILLGCGYPPFYSNHGLAISPGMKTRIRMGQYFPPNPWSEVSEEVKMLIRNLLKT 304

Db 229 LGVIMVILLGCGYPPFYSNHGLAISPGMKTRIRMGQYFPPNPWSEVSEEVKMLIRNLLKT 288

Qy 305 EPTQRMWTFMFNHPWIMQSTKVPQTPPLHTSRVLKEDKERWEDVKEEMTSALATMRVDYE 364

Db 289 EPTQRMWTFMFNHPWIMQSTKVPQTPPLHTSRVLKEDKERWEDVKEEMTSALATMRVDYE 348

Qy 365 QIKKIEDASNPILLKRRKK 385

Db 349 QIKKIEDASNPILLKRRKK 369

## RESULT 9

Q5XGX7\_XENLA

ID Q5XGX7\_XENLA PRELIMINARY; PRT; 374 AA.

AC Q5XGX7;

DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.

DT 07-FEB-2006, entry version 1.

DE LOC495118 protein.

GN Name=LOC495118;

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;





Qy 151 DQAFTEREASIMKSGEAIQYLSINIAHARDVDPENLLYTSKRPNAIKLTDGFAKET 210  
 D 151 DQAFTEREASIMKSGEAIQYLSINIAHARDVDPENLLYTSKRPNAIKLTDGFAKET 210  
 Db 121 DQAFTEREASIMKSGEAIQYLSINIAHARDVDPENLLYTSKRPNAIKLTDGFAKET 180  
 Qy 211 TSHNSLTTPCTPYVAVPEVLGPEKDKSCDMSGLGVIMYLLCGYPPFYNHGLAISPG 270  
 D 211 TSHNSLTTPCTPYVAVPEVLGPEKDKSCDMSGLGVIMYLLCGYPPFYNHGLAISPG 270  
 Db 181 TSHNSLTTPCTPYVAVPEVLGPEKDKSCDMSGLGVIMYLLCGYPPFYNHGLAISPG 240  
 Qy 271 MKTRIRMGQYFPPNPSEVEEVKMLIRNLKTEPTORTMTITFPMHHPWIMQSTKVPQT 330  
 D 271 MKTRIRMGQYFPPNPSEVEEVKMLIRNLKTEPTORTMTITFPMHHPWIMQSTKVPQT 330  
 Db 241 MKTRIRMGQYFPPNPSEVEEVKMLIRNLKTEPTORTMTITFPMHHPWIMQSTKVPQT 300  
 Qy 331 PLHTRSRVLKDKERWEDVKEEMTSALATMR 360  
 D 331 PLHTRSRVLKDKERWEDVKEEMTSALATMR 360  
 Db 301 PLHTRSRVLKDKERWEDVKEEMTSALATMR 330

RESULT 12  
 Q4SRAO TETNG PRELIMINARY; PRT; 340 AA.  
 AC Q4SRAO;  
 DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.  
 DT 19-JUL-2005, sequence version 1.  
 DE Chromosome 11 SCAF14528, whole genome shotgun sequence. (Fragment).  
 GN ORFNames=GSTENG0014009001;  
 OS Tetraodon nigroviridis (Green puffer).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
 OC Tetraodontidae; Tetraodontidae; Tetraodon.  
 OX NCBI\_TaxID=99883;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=15496914; DOI=10.1038/nature03025;  
 RA Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,  
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossaat C., Segurens B.,  
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
 RA Anthonard V., Jubin C., Castelli V., Katinka M., Vacherie B.,  
 RA Blomont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,  
 RA Parra G., Lardier G., Brottier P., Coutanceau J.-P., Gouzy J.,  
 RA Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,  
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,  
 RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.;  
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
 the early vertebrate proto-karyotype.";  
 RL Nature 431:946-957(2004).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RG Genoscope; Whitehead Institute Centre for Genome Research;  
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
 CC -!- CAUTION: The sequence shown here is derived from an  
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 preliminary data.  
 CC -!- FUNCTION: Plays a key role in the control of the eukaryotic cell  
 cycle. It is required in higher cells for entry into S-phase and  
 mitosis. Component of the kinase complex that phosphorylates the  
 repetitive C-terminus of RNA polymerase II. Catalytic component of  
 MPF (By similarity).  
 CC -!- SUBUNIT: Forms a stable but non-covalent complex with cyclin B in  
 mature oocytes (By similarity).  
 CC -----  
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 CC Distributed under the Creative Commons Attribution-NoDerivs License  
 CC -----  
 CC EMBL; CAE01014528; CAF96832.1; -; Genomic\_DNA.  
 DR GO:0005524; F:ATP binding; IEA.  
 DR GO:0000166; F:nucleotide binding; IEA.  
 DR GO:0004672; F:protein kinase activity; IEA.

DR GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro: IPR000719; Prot kinase.  
 DR InterPro: IPR002290; Ser Thr\_kinase.  
 DR Pfam: PF00069; Pkinase; 1.  
 DR ProDom: PD000001; Prot kinase; 1.  
 DR PROSITE: PS00107; PROTEIN KINASE ATP; UNKNOWN\_1.  
 DR PROSITE: PS00011; PROTEIN KINASE\_DOM; 1.  
 KW ATP-binding; Nucleotide-binding.  
 FT NON\_TER 1 340  
 FT NON\_TER 340 340  
 SQ SEQUENCE 340 AA; 39002 MW; 3FlF9438E154E3EC CRC64;  
 Query Match 69.7%; Score 1468; DB 2; Length 340;  
 Best Local Similarity 76.1%; Pred. No. 1e-77;  
 Matches 280; Conservative 22; Mismatches 34; Indels 32; Gaps 2;  
 Qy 22 PALPHPPAQPPP---PPQOPPOPHVKSGLQIKNAIIDYKYTSQVLGKINGKVLQIF 78  
 D 22 PALPHPPAQPPP---PPQOPPOPHVKSGLQIKNAIIDYKYTSQVLGKINGKVLQIF 78  
 Db 1 PLFPNPGGQONPTGQQNPGHFLPFPHARPSLQIKNAISDDYKVTSQVLGKINGKVLQIF 60  
 Qy 79 NKRTQEKFAKMLQDCPKARREVELHWRASOCPHIVRIVDYENLYAGRKCLLIVMECLD 138  
 D 79 NKRTQEKFAKMLQDCPKARREVELHWRASOCPHIVRIVDYENLYAGRKCLLIVMECLD 138  
 Db 61 HKKSADYALKMLQDCAKARREVELHWRASPCANIVRIIDYENLYOSRKCLLIVMECLD 120  
 Qy 139 GGELFSRIQDRGDOAFTEREASEIMKSGEAIQYLSINIAHARDVDPENLLYTSKRPNAI 198  
 D 139 GGELFSRIQDRGDOAFTEREASEIMKSGEAIQYLSINIAHARDVDPENLLYTSKRPNAI 198  
 Db 121 GGELFSRIQDRGDOAFTEREASEIMKSGEAIQYLSINIAHARDVDPENLLYTSKRPNAI 151  
 Qy 199 LKLTDFGFAKETTHNSLTTPCTPYVAVPEVLGPEKDKSCDMSGLGVIMYLLCGYPP 258  
 D 199 LKLTDFGFAKETTHNSLTTPCTPYVAVPEVLGPEKDKSCDMSGLGVIMYLLCGYPP 258  
 Db 152 LKLTDFGFAKETTHNSLTTPCTPYVAVPEVLGPEKDKSCDMSGLGVIMYLLCGYPP 211  
 Qy 259 FYSNHGLAISPGMKTRIRMGQYFPPNPSEVEEVKMLIRNLKTEPTORTMTITFPMNH 318  
 D 259 FYSNHGLAISPGMKTRIRMGQYFPPNPSEVEEVKMLIRNLKTEPTORTMTITFPMNH 318  
 Db 212 FYSNHGLAISPGMKTRIRMGQYFPPNPSEVEEVKMLIRNLKTEPTORTMTITFPMNH 271  
 Qy 319 PWIMQSTKVPQTPLHTRSRVLKDKERWEDVKEEMTSALATMRVDYEQIKIKIEDASNPL 378  
 D 319 PWIMQSTKVPQTPLHTRSRVLKDKERWEDVKEEMTSALATMRVDYEQIKIKIEDASNPL 378  
 Db 272 PWIMQSTKVPQTPLHTRSRVLKDKERWEDVKEEMTSALATMRVDYEQIKIKIEDASNPL 331  
 Qy 379 LLKRRKKA 386  
 D 379 LLKRRKKA 386  
 Db 332 LLKRRKKA 339

RESULT 13  
 MAPK3\_HUMAN STANDARD; PRT; 382 AA.  
 ID MAPK3\_HUMAN  
 AC Q16644;  
 DT 06-DEC-2005, integrated into UniProtKB/Swiss-Prot.  
 DT 01-NOV-1996, sequence version 1.  
 DT 07-MAR-2006, entry version 38.  
 DE MAP kinase-activated protein kinase 3 (EC 2.7.1.37) (MAPK-activated  
 DE protein kinase 3) (MAPKAP kinase 3) (MAPKAP-3) (Chromosome 3p kinase  
 DE (3pK).  
 GN Name=MAPKAPK3;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [MRNA], FUNCTION, TISSUE SPECIFICITY, AND  
 RP PHOSPHORYLATION  
 RX MEDLINE=96215257; PubMed=8626550; DOI=10.1074/jbc.271.14.8488;  
 RA McLaughlin M.M., Kumar S., McDonnell P.C., Van Horn S., Lee J.C.,  
 RA Livi G.P., Young P.R.;  
 RT "Identification of mitogen-activated protein (MAP) kinase-activated  
 RT protein kinase-3, a novel substrate of CSBP p38 MAP kinase.";  
 RL J. Biol. Chem. 271:8488-8492(1996).  
 RN [2]  
 RN NUCLEOTIDE SEQUENCE [MRNA], TISSUE SPECIFICITY, AND PHOSPHORYLATION.  
 RP TISSUE=Heart;







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RESULT 14
MAPK3 RAT
ID MAPK3 RAT STANDARD; PRT; 384 AA.
AC Q66H84;
DT 06-DEC-2005, integrated into UniProtKB/Swiss-Prot.
DT 11-OCT-2004, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE MAP kinase-activated protein kinase 3 (EC 2.7.1.37) (MAPK-activated
DE protein kinase 3) (MAPKAP kinase 3) (MAPKAPK-3).
GN Name=Mapkapk3;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Kidney;
RG NIH - Mammalian Gene Collection (MGC) project;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Modulator of polycomb-mediated repression, which can be
CC activated either by ERK, p38 and JNK. Substrate of CSBP (By
CC similarity).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBUNIT: Interacts with TCF3 and with polycomb proteins, such as
CC PCH2 and PCGF4 (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Predominantly
CC located in the nucleus, when activated it translocates to the
CC cytoplasm (By similarity).
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; BC081974; AAH81974.1; -; mRNA.
DR SRR; Q66H84; 37-338.
DR ENSEMBL; ENSRNOG0000014832; Rattus norvegicus.
DR RGD; 1304980; Mapkapk3.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Nuclear protein; Nucleotide-binding;
KW Phosphorylation; Serine/threonine-protein kinase; Transferase.
FT CHAIN 1 384
FT MAP kinase-activated protein kinase 3.
FT /FTID=PRO_0000086295.
FT DOMAIN 46 306
FT NP_BIND 52 60
FT ACT_SITE 168 168
FT BINDING 75 75
FT SEQUENCE 384 AA; 43222 MW; E094358C901F7E70 CRC64;
Query Match 65.1%; Score 1371; DB 1; Length 384;
Best Local Similarity 68.7%; Pred. No. 5.2e-72;
Matches 261; Conservative 53; Mismatches 48; Indels 18; Gaps 4;
Qy 17 PGP---PTPALPHPPAPPPPPPPQPFQFHVKSLGLOIKNAIIDYKVTQSVILGLGNGK 73
Db 14 PQPGALGAPALGGAPA-----PGVREP-----KKYAVTDYQLSKQVGLGVNGK 59
Qy 74 VLQIFKRTQKQKMLQDCPKARREVELHWRASQCPHIVRIVDVYENLYAGRKCLLIV 133
Db 60 VLECYHRRSGQKCALKLLYDSFKARQEVDDHWQASGGPHIVRIIDVTENMHGKCLLIV 119
Qy 134 MECLDGGELFSRIQDRGDQAFTEREASEIMKSGEAIQYLHSHINIAHRDVKPENLYTSK 193
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Db 120 MECMEGGELFSRIQDRGDQAFTEREAAEINRDICTAIOFLHSQNIARHVDKVENLLYTSK 179
Qy 194 RPNAILKLTDFGFAKETTSNLSLTTPCYTPYVVAPEVLGPEKYDKSCDMNSLGVIMYILL 253
Db 180 EKDAVLKLTDFGFAKETT-QNALQTPCYTPYVVAPEVLGPEKYDKSCDMNSLGVIMYILL 238
Qy 254 CGYPPFYSNHGLAISPGMKTRIRMGQYEFNPENPEVSEEVKMLIRLLKLTQPTQRMIT 313
Db 239 CGFPFPYSNTGOALSPGMKRRIRLGGYCPKPEWADYSEDAKQLIRLLKLTQPTQLT 298
Qy 314 EFMNHPWIMOSTKVPQTPPLTSRVLKEDEKEDVSEKEMTSALATMRVDYEQIKKIED 373
Db 299 QFMNHPWINSMEVPTPLHTARVLEEDKQHDVDEKEMTSALATMRVDYDQVKIKDLKT 358
Qy 374 ASNPILLKRRKKARALEAAA 393
Db 359 SNRLNKKRRKKGGSSAS 378

RESULT 15
MAPK3 BOVIN
ID MAPK3_BOVIN STANDARD; PRT; 384 AA.
AC Q3SYZ2;
DT 06-DEC-2005, integrated into UniProtKB/Swiss-Prot.
DT 11-OCT-2005, sequence version 1.
DT 07-MAR-2006, entry version 7.
DE MAP kinase-activated protein kinase 3 (EC 2.7.1.37) (MAPK-activated
DE protein kinase 3) (MAPKAP kinase 3) (MAPKAPK-3).
GN Name=MAPKAPK3;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=Crossbred X Angus; TISSUE=ileum;
RG NIH - Mammalian Gene Collection (MGC) project;
RL Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Modulator of polycomb-mediated repression, which can be
CC activated either by ERK, p38 and JNK. Substrate of CSBP (By
CC similarity).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBUNIT: Interacts with TCF3 and with polycomb proteins, such as
CC PCH2 and PCGF4 (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Predominantly
CC located in the nucleus, when activated it translocates to the
CC cytoplasm (By similarity).
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
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CC -----
DR EMBL; BC103321; AA103322.1; -; mRNA.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Nuclear protein; Nucleotide-binding;
KW Phosphorylation; Serine/threonine-protein kinase; Transferase.
FT CHAIN 1 384
FT MAP kinase-activated protein kinase 3.
FT /FTID=PRO_0000086292.
FT DOMAIN 46 306
FT NP_BIND 52 60
FT ACT_SITE 168 168
FT BINDING 75 75
FT SEQUENCE 384 AA; 43222 MW; E094358C901F7E70 CRC64;
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SQ SEQUENCE 384 AA; 43316 MW; C9D737DDCF8A0C06 CRC64;
Query Match 65.1%; Score 1370; DB 1; Length 384;
Best Local Similarity 70.8%; Pred. No. 5.9e-72;
Matches 257; Conservative 50; Mismatches 48; Indels 8; Gaps 2;

Qy 30 QPPPPPPQPPQPFHVKSGL-----QIKKNAIIDDYKVTSQLGLGINKVLQIFNKRT 82
Db 9 QGGPAPPSPGVPCGPCSAGAPALGGRREPKKYAVTDDYQLSKQVLGLGVNGKVLCECFHRT 68

Qy 83 QEKFALAKMLQDCPKARREVELHWEASOCPHIVRIVDVVENLYAGRKCLLIIVMECLDGEL 142
Db 69 GQKCALKLLYDSPKARQEVDDHHWQSGPHIVRLDVFNHHSKRCLLIIMECEGEL 128

Qy 143 FSRIQDRGDOAFTEREASEIMKSIGEAIQYLHSINIAHRDVKPENLYTSKRPNAILKLT 202
Db 129 FSRIQERGDQAFTEREAAEIMRDIGTAIQFLHSRNIAHRDVKPENLYTSKDXDAVLKLT 188

Qy 203 DFGPAKETTSNSLTTCYTPYYVAPEVLGPEKYDKSCDMWSLGVIMYILLCGYPPFYSN 262
Db 189 DFGPAKETT-QNALQTPCYTPYYVAPEVLGPEKYDKSCDMWSLGVIMYILLCGFPPFYSN 247

Qy 263 HGLAISPGMKTRIRMGQYEPFNPSEVSEVKMLIRNLLKTEPTORMTITEFNNHPWIM 322
Db 248 TGQAISPGMKRRIRLGOIGFPSPSEVSEDAKQILRLLLKTDPIERLTITQFNHWPIN 307

Qy 323 QSTKVPQTPHLTSRVLKEDKERNEDVKEEMTSALATMRVDYEQIKIKKIEDASNPLLLKR 382
Db 308 QSMVVPQTPPLHTARVLQEDRDHDHDEVKEEMTSALATMRVDYDQVKIKDLKTSNNRLLNKR 367

Qy 383 RKK 385
Db 368 RKK 370
```

Search completed: June 19, 2006, 08:59:49  
Job time : 300 secs



QY 361 VDYEQIKIKKIEDASNP... 396  
Db 361 VDYEQIKIKKIEDASNP... 396

RESULT 2  
S78100  
MAPK-activated protein kinase (EC 2.7.1.-) 2 - mouse (fragment)  
N;Alternate names: MAPKAP kinase 2; mitogen-activated protein kinase-activated protein kinase  
C;Species: Mus musculus (house mouse)  
C;Date: 29-Jan-1998 #sequence\_revision 06-Feb-1998 #text\_change 09-Jul-2004  
C;Accession: S78100; S39472  
R;Gaestel, M.  
Submitted to the EMBL Data Library, November 1995  
A;Description: The MAP kinase-activated protein kinase 2 contains a proline-rich SH3-binding domain.  
A;Reference number: S78100  
A;Accession: S78100  
A;Molecule type: mRNA  
A;Residues: 1-385 <GAE>  
A;Cross-references: UNIPROT:P49138; UNIPARC:UPI00000277C0; EMBL:X76850; NID:g1089895; P1089895  
A;Experimental source: lung  
A;Note: this is a revision to the sequence from reference S39472  
R;Engel, K.; Plath, K.; Gaestel, M.  
FEBS Lett 336, 143-147, 1993  
A;Title: The MAP kinase-activated protein kinase 2 contains a proline-rich SH3-binding domain.  
A;Reference number: S39472; MUID:94085571; PMID:8262198  
A;Accession: S39472  
A;Molecule type: mRNA  
A;Residues: 3-196, 'R', 198-250, 'K', 252-260, 'N', 262-385 <ENG>  
A;Cross-references: UNIPARC:UPI0000175568; EMBL:X76850  
A;Note: this sequence has been revised in reference S78100  
C;Superfamily: kinase-related transforming protein; protein kinase homology  
C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein kinase  
F;9-27/Region: proline-rich  
F;21-29/Region: SH3-binding motif  
F;46-310/Domain: protein kinase homology <KIN>  
F;55-63/Region: protein kinase ATP-binding motif  
F;370-374/Region: nuclear location signal  
F;319/Binding site: phosphate (Thr) (covalent) (by MAP kinase) #status predicted

Query Match 91.2%; Score 1921; DB 2; Length 385;  
Best Local Similarity 92.7%; Pred. No. 5.3e-77;  
Matches 367; Conservative 7; Mismatches 8; Indels 14; Gaps 2;

QY 1 SQGSPVPVPAPAPPQPPPTPALPHPPAQP... 60  
Db 4 SPQTPPAPFPSPPPP-----APAPPPP... 49

QY 61 VTSQVLGLINGKVLQIFNKRTOEKFKAL... 120  
Db 50 VTSQVLGLINGKVLQIFNKRTOEKFKAL... 109

QY 121 ENLYAGRKCLLIWVECLDGGELFSRIQDRG... 180  
Db 110 ENLYAGRKCLLIWVECLDGGELFSRIQDRG... 169

QY 181 RDVKPENLLYTSKRPNAILKLTDFGFAKET... 240  
Db 170 RDVKPENLLYTSKRPNAILKLTDFGFAKET... 229

QY 241 DMNSLGVIMVILLCGYPFYSNHGLAISPGMK... 300  
Db 230 DMNSLGVIMVILLCGYPFYSNHGLAISPGMK... 289

QY 301 LLKTEPTQRMITTEFNNHPWIMQSTKVPO... 360  
Db 290 LLKTEPTQRMITTEFNNHPWIMQSTKVPO... 349

QY 361 VDYEQIKIKKIEDASNP... 396  
Db 350 VDYEQIKIKKIEDASNP... 385

RESULT 3  
JC2204  
MAPK-activated protein kinase (EC 2.7.1.-) 2 - human  
N;Alternate names: MAPKAP kinase 2  
C;Species: Homo sapiens (man)  
C;Date: 28-Aug-1985 #sequence\_revision 07-Oct-1994 #text\_change 09-Jul-2004  
C;Accession: JC2204  
R;Zu, Y.L.; Wu, F.; Gilchrist, A.; Ai, Y.; Labadia, M.E.; Huang, C.K.  
Biochem. Biophys. Res. Commun. 200, 1118-1124, 1994  
A;Title: The primary structure of a human map kinase activated protein kinase 2.  
A;Reference number: JC2204; MUID:94235003; PMID:8179591  
A;Accession: JC2204  
A;Molecule type: mRNA  
A;Residues: 1-370 <ZUY>  
A;Cross-references: UNIPROT:P49137; UNIPARC:UPI000002AE18; GB:U12779; NID:g530089; PIDN:1089895  
A;Experimental source: HL-60 cell  
A;Superfamily: kinase-related transforming protein; protein kinase homology  
C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein kinase  
F;10-40/Region: proline-rich  
F;32-40/Region: SH3-binding motif  
F;61-325/Domain: protein kinase homology <KIN>  
F;70-78/Region: protein kinase ATP-binding motif  
F;334/Binding site: phosphate (Thr) (covalent) (by MAP kinase) #status predicted

Query Match 89.4%; Score 1882; DB 2; Length 370;  
Best Local Similarity 100.0%; Pred. No. 2.5e-75;  
Matches 349; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQGSPVPVPAPAPPQPPPTPALPHPPAQP... 60  
Db 5 SQGSPVPVPAPAPPQPPPTPALPHPPAQP... 64

QY 61 VTSQVLGLINGKVLQIFNKRTOEKFKAL... 120  
Db 65 VTSQVLGLINGKVLQIFNKRTOEKFKAL... 124

QY 121 ENLYAGRKCLLIWVECLDGGELFSRIQDRG... 180  
Db 125 ENLYAGRKCLLIWVECLDGGELFSRIQDRG... 184

QY 181 RDVKPENLLYTSKRPNAILKLTDFGFAKET... 240  
Db 185 RDVKPENLLYTSKRPNAILKLTDFGFAKET... 244

QY 241 DMNSLGVIMVILLCGYPFYSNHGLAISPGMK... 300  
Db 245 DMNSLGVIMVILLCGYPFYSNHGLAISPGMK... 304

QY 301 LLKTEPTQRMITTEFNNHPWIMQSTKVPO... 349  
Db 305 LLKTEPTQRMITTEFNNHPWIMQSTKVPO... 353

RESULT 4  
S49490  
MAPK-activated protein kinase 2 (EC 2.7.1.-) - long-tailed hamster (fragment)  
N;Alternate names: MAPKAP kinase 2; mitogen-activated protein kinase-activated protein kinase  
C;Species: Cricetus longicaudatus (long-tailed hamster)  
C;Date: 20-Feb-1995 #sequence\_revision 12-Dec-1997 #text\_change 09-Jul-2004  
C;Accession: S49490  
R;Huot, J.; Lambert, H.; Lavoie, J.N.; Guimond, A.; Houle, F.; Landry, J.  
submitted to the EMBL Data Library, October 1994  
A;Description: Characterization of p45-54 hep27 kinase, a stress sensitive kinase which is induced by proinflammatory cytokines.  
A;Reference number: S49490  
A;Accession: S49490  
A;Molecule type: mRNA  
A;Residues: 1-329 <HUO>  
A;Cross-references: UNIPROT:P49136; UNIPARC:UPI000012F196; EMBL:X82220; NID:g559434; PIDN:1089895  
A;Experimental source: ovary  
C;Superfamily: kinase-related transforming protein; protein kinase homology  
C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein kinase  
F;1-254/Domain: protein kinase homology (fragment) <KIN>  
F;314-318/Region: nuclear location signal

F;263/Binding site: phosphate (Thr) (covalent) (by MAP kinase) #status predicted

Query Match 81.1%; Score 1709; DB 2; Length 329;  
Best Local Similarity 98.5%; Pred. No. 7.2e-68;  
Matches 324; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 68 LGINGKVLQIFNKRQTEKFAKMLQDCPKARREVELHWRASQCPHIVRVDVYENLYAGR 127  
Db 1 LGINGKVLRIFDKRTQOKFALKMLQDCPKARREVELHWRASQCPHIVRVDVYENLYAGR 60  
Qy 128 KCLLIIVMECLDGGELFSRIQDRGDAFTEREASEIMKSGEAIQYLHSINTAHRDVKPEN 187  
Db 61 KCLLIIVMECLDGGELFSRIQDRGDAFTEREASEIMKSGEAIQYLHSINTAHRDVKPEN 120  
Qy 188 LLYTSKRPNAILKLTDFGFAKETTSNLSLTTPCTPYVVAPEVLGPEKYDKSCDMWSLGV 247  
Db 121 LLYTSKRPNAILKLTDFGFAKETTSNLSLTTPCTPYVVAPEVLGPEKYDKSCDMWSLGV 180  
Qy 248 IMYILLCGYPFFYNNHGLAISPGMKTRIRMGQYFFPNPWESEVSEVVKMLIRNLLKTEPT 307  
Db 181 IMYILLCGYPFFYNNHGLAISPGMKTRIRMGQYFFPNPWESEVSEVVKMLIRNLLKTEPT 240  
Qy 308 QRMWTFPMNHPWIMQSTKVPQTLHTSRVLKEDKERWEDYKEEMTSALATMRVDYQIK 367  
Db 241 QRMWTFPMNHPWIMQSTKVPQTLHTSRVLKEDKERWEDYKEEMTSALATMRVDYQIK 300  
Qy 368 IKKTEDASNPLLLKRRKKARALEAAALAH 396  
Db 301 IKKTEDASNPLLLKRRKKARALEAAALAH 329

## RESULT 5

JC6094

MAPK-activated protein kinase (EC 2.7.1.1-) 3 - human

N;Alternate names: mitogen-activated protein kinase-activated protein kinase 3pk

C;Species: Homo sapiens (man)

C;Date: 18-Feb-2000 #sequence\_revision 18-Feb-2000 #text\_change 09-Jul-2004

C;Accession: JC6094

R;Sithanandam, G.; Latif, F.; Duh, F.M.; Bernal, R.; Smola, U.; Li, H.; Kuzmin, I.; Wixl

R.; Dean, M.; Klein, G.; Lerman, M.I.; Minna, J.D.; Rapp, U.R.; Allikmets, R.

Mol. Cell. Biol. 16, 868-876, 1996

A;Title: 3pk, a new mitogen-activated protein kinase-activated protein kinase located in

A;Reference number: JC6094; MUID:96182089; PMID:8622688

A;Accession: JC6094

A;Molecule type: mRNA

A;Residues: 1-382 &lt;SIT&gt;

A;Cross-references: UNIPROT:Q16644; UNIPARC:UPI0000073D7E; GB:U09578; NID:g1209017; PIDN

A;Experimental source: heart

C;Genetics:

A;Gene: GDB:MAPKAP; 3pk

A;Cross-references: GDB:6175915

A;Map position: 3p21.3

C;Superfamily: kinase-related transforming protein; protein kinase homology

C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein k

F;12-16/Region: proline-rich

F;41-304/Domain: protein kinase homology &lt;KIN&gt;

F;50-58/Region: protein kinase ATP-binding motif

F;364-368/Region: nuclear location signal

F;3/3/Binding site: phosphate (Thr) (covalent) (by MAP kinase) #status predicted

Query Match 66.0%; Score 1391; DB 1; Length 382;  
Best Local Similarity 67.4%; Pred. No. 5.2e-54;  
Matches 265; Conservative 50; Mismatches 56; Indels 22; Gaps 3;

Qy 1 SQGSPVPVFPAPAPPQPTPALPHPPAQPPPPPPQFPQFHVKSGLQIKKNAIIDDYK 60  
Db 6 AEQGGPVP-----PPVAPGGPLGGAPGGRREP-----KKYAVTDDYQ 44

Qy 61 VTSQVLGINGKVLQIFNKRQTEKFAKMLQDCPKARREVELHWRASQCPHIVRVDVY 120  
Db 45 LSKQVLGVLGVNGKVLQTECFHRTGTGKCALKLYDSPKARQEVDDHHWQSGGPHIVCILDVY 104

Qy 121 ENLYAGRKCLLIIVMECLDGGELFSRIQDRGDAFTEREASEIMKSGEAIQYLHSINIAH 180

Db 105 ENMHGKRCLLIIVMECLDGGELFSRIQDRGDAFTEREAAEIMRDICTAIOFLHSHNIAH 164  
Qy 181 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSNLSLTTPCTPYVVAPEVLGPEKYDKSC 240  
Db 165 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSNLSLTTPCTPYVVAPEVLGPEKYDKSC 223  
Qy 241 DMWSLGVIMYILLCGYPFFYNNHGLAISPGMKTRIRMGQYFFPNPWESEVSEVVKMLIRN 300  
Db 224 DMWSLGVIMYILLCGYPFFYNNHGLAISPGMKTRIRMGQYFFPNPWESEVSEVVKMLIRN 283  
Qy 301 LLKTEPTQRMWTFPMNHPWIMQSTKVPQTLHTSRVLKEDKERWEDYKEEMTSALATMR 360  
Db 284 LLKTDPTERLTIITQFMNHPWIMQSMVVPQTLHTARVLQEDKHQWDEKSEMTSALATMR 343  
Qy 361 VDYEQIKIKKIEDASNPLLLKRRKKARALEAAA 393  
Db 344 VDQDVKIKDKLTSNNLLNKKRRKKQAGSSAS 376

## RESULT 6

S39794

MAPK-activated protein kinase 2 (EC 2.7.1.1-) - rabbit (fragment)

N;Alternate names: MAPKAP kinase 2; mitogen-activated protein kinase-activated protein kinase

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 07-Oct-1994 #sequence\_revision 12-Dec-1997 #text\_change 09-Jul-2004

C;Accession: S39794

R;Stokoe, D.; Caudwell, B.; Cohen, P.T.W.; Cohen, P.

Biochem. J. 296, 843-849, 1993

A;Title: The substrate specificity and structure of mitogen-activated protein (MAP) kinase

A;Reference number: S39793; MUID:94107253; PMID:8280084

A;Accession: S39794

A;Molecule type: mRNA

A;Residues: 1-256 &lt;STO&gt;

A;Cross-references: UNIPROT:P49139; UNIPARC:UPI000016C586; ENBL:X75345; NID:g407067; PIDN

A;Note: the authors translated the codon CAC for residue 82 as Asp

C;Superfamily: kinase-related transforming protein; protein kinase homology

C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein kinase

F;1-6/Region: proline-rich (fragment)

F;27-256/Domain: protein kinase homology (fragment) &lt;KIN&gt;

Query Match 64.0%; Score 1347; DB 2; Length 256;  
Best Local Similarity 98.0%; Pred. No. 2.9e-52;  
Matches 251; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 31 PPPPPQPPQPPQFHVRSGLQIKKNAIDDDYKVTQVGLGINGKVLQIFNKRQTEKFAKLM 90  
Db 1 PPPPPQPPQPPQFHVRSGLQIKKNAIDDDYKVTQVGLGINGKVLQIFNKRQTEKFAKLM 60

Qy 91 LQDCPKARREVELHWRASQCPHIVRVDVYENLYAGRKCLLIIVMECLDGGELFSRIQDRG 150  
Db 61 LQDCPKARREVELHWRASQCPHIVRVDVYENLYAGRKCLLIIVMECLDGGELFSRIQDRG 120

Qy 151 DQAFTEREASEIMKSGEAIQYLHSINIAHRDVKPENLLYTSKRPNAILKLTDFGFAKET 210  
Db 121 DQAFTEREASEIMKSGEAIQYLHSINIAHRDVKPENLLYTSKRPNAILKLTDFGFAKET 180

Qy 211 TSHNSLTTPCTPYVVAPEVLGPEKYDKSCDMWSLGVIMYILLCGYPFFYNNHGLAISPG 270  
Db 181 TSHNSLTTPCTPYVVAPEVLGPEKYDKSCDMWSLGVIMYILLCGYPFFYNNHGLAISPG 240

Qy 271 MKTRIRMGQYFFNPPE 286  
Db 241 MKTRIRMGQYFFNPPE 256

## RESULT 7

JC4297

MAPK-activated protein kinase (EC 2.7.1.1-) 2 - fruit fly (Drosophila melanogaster)

N;Alternate names: MAPKAPK-2; mitogen-activated protein kinase-activated protein kinase

C;Species: Drosophila melanogaster

C;Date: 16-Nov-1995 #sequence\_revision 08-Feb-1996 #text\_change 09-Jul-2004

C;Accession: JC4297









C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 05-Oct-2004  
C;Accession: S50193; A49682; A46038  
R;Cho, F.S.; Phillips, K.S.; Bogucki, B.; Weaver, T.E.  
Biochim. Biophys. Acta 1224: 156-160, 1994  
A;Title: Characterization of a rat cDNA clone encoding calcium/calmodulin-dependent protein kinase I  
A;Reference number: S50193; MUID:95035115; PMID:7948038  
A;Accession: S50193  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-374 <CHO>  
A;Cross-references: UNIPROT:Q63450; UNIPARC:UPI000012DC8A; EMBL:L26288; NID:9439613; PID:R;Picciotto, M.R.; Czernik, A.J.; Nairn, A.C.  
J. Biol. Chem. 268: 26512-26521, 1993  
A;Title: Calcium/calmodulin-dependent protein kinase I. cDNA cloning and identification  
A;Reference number: A49682; MUID:94075341; PMID:8253780  
A;Accession: A49682  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-111, 'G', 113-117, 'R', 119-308, 'R', 310-322, 'HQFG', 327, 'T', 329, 'TDS', <PIC>  
A;Cross-references: UNIPARC:UPI0000170ADA; GB:L24907; NID:g406112; PIDN:AAA19670.1; PID:R;Mochizuki, H.; Ito, T.; Hidaka, H.  
J. Biol. Chem. 268: 9143-9147, 1993  
A;Title: Purification and characterization of Ca2+/calmodulin-dependent protein kinase V  
A;Reference number: A46038; MUID:93232082; PMID:8386178  
A;Accession: A46038  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 12-36, 'T', <MOC>  
A;Cross-references: UNIPARC:UPI00000E82D2  
A;Experimental source: cerebrum  
A;Note: sequence extracted from NCBI backbone (NCBI:129927)  
C;Superfamily: Calcium/calmodulin-dependent protein kinase type I; protein kinase homolog  
C;Keywords: ATP; autophosphorylation; calmodulin binding; phosphoprotein; phosphotransferase  
F:18-276/Domain: protein kinase homology <KIN>  
F:26-34/Region: protein kinase ATP-binding motif  
F:293-299/Region: autoinhibitory  
F:302-314/Region: calmodulin binding  
F:177/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted

Query Match	24.4%	Score 514.5	DB 1	Length 374
Best Local Similarity	36.4%	Pred. No. 5.5e-16		
Matches 117	Conservative 69	Mismatches 94	Indels 41	Gaps 12
Qy	56	IDDYKVTSQLGLGNGKVLQIFNKRTQEKPAKMLQDCPKARREVE-----L	103	
Db	19	IYDFR---DVLGTGAFSEVILAEKRTQKLVAKICI-----AKKALSGKSGSMENETAVL	70	
Qy	104	HWRASQCPHIVRIVDVYENLVYGRKCLLIVMCELDGGELFSRIQDRGDAQTEREASEIM	163	
Db	71	H--KIKHPNIVALDDIVES--GGH--LYLIQMLVSGGELFDRIVEKG--FYTERDASRLI	122	
Qy	164	KSIGEALQYLSINIAHRDVKPENLLYTSKRPNAILKLTDPGFAKETTSNLSLTTCYTP	223	
Db	123	FQVLDAVKYLDHGLGVHRDLKPNLLYSLDEDSKIMISDFGLSKMEDPGSVLSTACGTP	182	
Qy	224	YVVAPEVLGPKYDKSCDMWSLGVIMYILLCGYPPFYNSHGLAISPGMKTRIRMGQYEPF	283	
Db	183	GYVAPEVLAQPKYSKAVDCWSIGVIAVILLCGYPPFYDENDAKLF----EQILKAEYEFD	238	
Qy	284	NPEWSEVSEVKMLIRNLLKTEPTQRTITFEMNHPIMOSTKVPQTPPLH--TSRVLKED	341	
Db	239	SPYWDIDSDSAKDFIRHLMKEDPKRFTEQALQHPWIAGDTALDKN-IHQSVSEQIKKN	297	
Qy	342	--KERWEDVKEEMTSALATMR	360	
Db	298	FAKSKW-----KQAFNATAVVR	314	

Search completed: June 19, 2006, 09:00:35  
Job time : 42 secs

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121 CAGTTCACGTCAAGTCCGGCCTGCAGATCAAGAAGACGCCATCATCGACTACAAG 180 QY













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Db 1411 GACAAGGAGCGGTGGGAGGATGTCAAGGGG 1440
|||||
Db 1411 GACAAGGAGCGGTGGGAGGATGTCAAGGGG 1440

RESULT 8
US-10-843-641A-5564
; Sequence 5564, Application US/10843641A
; Publication No. US20050064454A1
; GENERAL INFORMATION:
; APPLICANT: Avalon Pharmaceuticals, Inc.
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; FILE REFERENCE: 689290-189
; CURRENT FILING DATE: 2004-05-12
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: US/09/873,367
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US/09/954,531
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,436
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,832
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/964,824
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/09/967,768
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/09/968,007
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,347
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,708
; PRIOR FILING DATE: 2001-10-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 8447
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5564
; LENGTH: 2258
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-843-641A-5564

Query Match 88.0%; Score 1048.4; DB 10; Length 2258;
Best Local Similarity 99.9%; Pred. No. 7.5e-299;
Matches 1049; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCCAGGCGCAGAGCCCGCGGTGCCGTTCCTCCCGCCCGCCCGCGCGCGAGCCCCC 60
Db 391 TCCAGGCGCAGAGCCCGCGGTGCCGTTCCTCCCGCCCGCCCGCGCGAGCCCCC 450
QY 61 ACCCTGCCCTGCCGACCCCGCGCGAGCCCGCGCGCGCGCGCGAGTTCCCG 120
Db 451 ACCCTGCCCTGCCGACCCCGCGCGAGCCCGCGCGCGCGCGAGTTCCCG 510
QY 121 CAGTTCACGTCAAGTCGGCGCTGCAGATCAAGAAGACCCATCATCATGACTACAAG 180
Db 511 CAGTTCACGTCAAGTCGGCGCTGCAGATCAAGAAGACCCATCATCATGACTACAAG 570
QY 181 GTCACAGCAGGATCTCTGGGGTGGGCATCAACGGCAAAAGTTTTCAGATCTTCAACAAG 240
Db 571 GTCACAGCAGGATCTCTGGGGTGGGCATCAACGGCAAAAGTTTTCAGATCTTCAACAAG 630
QY 241 AGGACCCAGGAGAAATTCGGCTCAAAATGCTTCAGACTGCCCGCCAGGCCCGCAGGAG 300
Db 631 AGGACCCAGGAGAAATTCGGCTCAAAATGCTTCAGACTGCCCGCCAGGCCCGCAGGAG 690
QY 301 GTGGAGCTGCATGGCGGGCTCCAGTGCAGTGCAGATCGTGGATGTGTAC 360
Db 691 GTGGAGCTGCATGGCGGGCTCCAGTGCAGTGCAGATCGTGGATGTGTAC 750
QY 361 GAGAATCTGTACGAGGAGGAAGTGCCTGCTGATTGTTCATGGAATGTTTGGACGTTGA 420
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Db 751 GAGAACTGTACGAGGAGGAAGTGCCTGCTGCTATTGTTCATGAAATGTTTGGACGGTGA 810
QY 421 GAACTCTTTAGCCGAATCCAGGATCCAGGAGACAGGAGATTCACAGAAAGAGAGCATCC 480
Db 811 GAACTCTTTAGCCGAATCCAGGATCCAGGAGACAGGAGATTCACAGAAAGAGAGCATCC 870
QY 481 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGATTTCAATCAACATTTGCCAT 540
Db 871 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGATTTCAATCAACATTTGCCAT 930
QY 541 CGGGATGTCGAAGCCTGAGAATCTCTTATACACCTCCAAAAGGCCCAACGCGCATCTCTGAAA 600
Db 931 CGGGATGTCGAAGCCTGAGAATCTCTTATACACCTCCAAAAGGCCCAACGCGCATCTCTGAAA 990
QY 601 CTCACCTGACTTTGGCTTTGCCAAGGAACCCACGAGCACAACTCTTTGACCACTCTCTGT 660
Db 991 CTCACCTGACTTTGGCTTTGCCAAGGAACCCACGAGCACAACTCTTTGACCACTCTCTGT 1050
QY 661 TATACACCGTACTATGCTGGCTCCAGAAAGTCTGGGTCCAGAGAGTATGACAAAGTCTCTGT 720
Db 1051 TATACACCGTACTATGCTGGCTCCAGAAAGTCTGGGTCCAGAGAGTATGACAAAGTCTCTGT 1110
QY 721 GACATGCTGCTCCTGGGTGTCATGATCATCTGCTGTGCTGGGTATCCCCCTTCTAC 780
Db 1111 GACATGCTGCTCCTGGGTGTCATGATCATCTGCTGTGCTGGGTATCCCCCTTCTAC 1170
QY 781 TCCAAACCGGCTTCCCATCTCTCCGGGATGAAGACTCGCATCCGAATGGGCCAGTAT 840
Db 1171 TCCAAACCGGCTTCCCATCTCTCCGGGATGAAGACTCGCATCCGAATGGGCCAGTAT 1230
QY 841 GAATTTCCCAACCCAGAGTGTCCAGAAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT 900
Db 1231 GAATTTCCCAACCCAGAGTGTCCAGAAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT 1290
QY 901 CTGCTGAAAACAGAGCCCAACCCAGAGATGACCATCACCAGTTTATGAACCAACCTTGG 960
Db 1291 CTGCTGAAAACAGAGCCCAACCCAGAGATGACCATCACCAGTTTATGAACCAACCTTGG 1350
QY 961 ATCATGCAATCAACAAAGTTCCTCAACCCCATCTCAGACCAAGCGGGTCTCTGAAGAG 1020
Db 1351 ATCATGCAATCAACAAAGTTCCTCAACCCCATCTCAGACCAAGCGGGTCTCTGAAGAG 1410
QY 1021 GACAAGGAGCGGTGGGAGGATGTCAAGGAG 1050
Db 1411 GACAAGGAGCGGTGGGAGGATGTCAAGGGG 1440

RESULT 9
US-10-081-119-33
; Sequence 33, Application US/10081119
; Publication No. US20030045491A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; APPLICANT: Chan, Vivien W.
; TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic
; FILE REFERENCE: 16932.002
; CURRENT APPLICATION NUMBER: US/10/081,119
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/289,813
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 2263
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (379)...(1491)
US-10-081-119-33
```



```
Qy 661 TATACACCGTACTATGTGGCTCCAGAAAGTGTGGTCCAGAGAAAGTATGACAAAGTCTGT 720
Db 1051 TATACACCGTACTATGTGGCTCCAGAAAGTGTGGTCCAGAGAAAGTATGACAAAGTCTGT 1110
Qy 721 GACATGTGGTCCCTGGGTGTCATCATGTACATCTGTCTGTGTGGTATCCCTTCTAC 780
Db 1111 GACATGTGGTCCCTGGGTGTCATCATGTACATCTGTCTGTGTGGTATCCCTTCTAC 1170
Qy 781 TCCAAACACGCGCTTGCATCTCTCCGGGATGAAGACTCGCATCCGAATGGGCGAGTAT 840
Db 1171 TCCAAACACGCGCTTGCATCTCTCCGGGATGAAGACTCGCATCCGAATGGGCGAGTAT 1230
Qy 841 GAATTTCCCAACCCAGAAATGGTCAAGAGTATCAGAGAAAGTGAAGATGCTCATTCGGAAT 900
Db 1231 GAATTTCCCAACCCAGAAATGGTCAAGAGTATCAGAGAAAGTGAAGATGCTCATTCGGAAT 1290
Qy 901 CTGCTGAAGACAGAGCCCAAGAGTATGACCAATGACCAATGACCAATGACCAATGACCAATG 960
Db 1291 CTGCTGAAGACAGAGCCCAAGAGTATGACCAATGACCAATGACCAATGACCAATGACCAATG 1350
Qy 961 ATCATGCAATCAACAAAGTCCCTCAACCCCACTGCACACCAAGCGGGTCTTGAAGGAG 1020
Db 1351 ATCATGCAATCAACAAAGTCCCTCAACCCCACTGCACACCAAGCGGGTCTTGAAGGAG 1410
Qy 1021 GACAAGAGCGGTGGGAGGATGCAAGGAG 1050
Db 1411 GACAAGAGCGGTGGGAGGATGCAAGGAG 1440
```

## RESULT 11

```
US-10-951-389-33
; Sequence 33, Application US/10951389
; Publication No. US20050058627A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; APPLICANT: Chan, Vivien W.
; TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic
; FILE REFERENCE: 16932.002
; CURRENT APPLICATION NUMBER: US/10/951,389
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US/10/081,119
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/289,813
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 2263
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (379) ... (1491)
US-10-951-389-33
```

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Query Match 88.0%; Score 1048.4; DB 10; Length 2263;
Best Local Similarity 99.9%; Pred. No. 7.5e-299;
Matches 1049; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 1 TCCAGGGCCAGAGCCCGGTCGCGGTTCCTCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCG 60
Db 391 TCCAGGGCCAGAGCCCGGTCGCGGTTCCTCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCG 450
Qy 61 ACCCTGCGCTGCGGACCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCG 120
Db 451 ACCCTGCGCTGCGGACCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCG 510
Qy 121 CAGTTCACGTCAAGTCCGCTGACATCAAGAACGCCATCATCATGACTACAG 180
Db 511 CAGTTCACGTCAAGTCCGCTGACATCAAGAACGCCATCATCATGACTACAG 570
```

```
Qy 181 GTCAACAGCCAGCTCTCGGGCTGGGCATCAACGGCAAAAGTTTTCAGAGATCTTCAACAAG 240
Db 571 GTCAACAGCCAGCTCTCGGGCTGGGCATCAACGGCAAAAGTTTTCAGAGATCTTCAACAAG 630
Qy 241 AGGACCCAGAGAAATTTGCCCTCAAATGCTTTCAGAGCTGCCCCAAGAGCCCGCAGGGAG 300
Db 631 AGGACCCAGAGAAATTTGCCCTCAAATGCTTTCAGAGCTGCCCCAAGAGCCCGCAGGGAG 690
Qy 301 GTGAGCTGACCTGGGGGCTCCAGTGCCTCCAGTGCCTCCAGTGCCTCCAGTGCCTCCAGTGCCT 360
Db 691 GTGAGCTGACCTGGGGGCTCCAGTGCCTCCAGTGCCTCCAGTGCCTCCAGTGCCTCCAGTGCCT 750
Qy 361 GAGAATCTGTACGACGAGGAGAAAGTGCCTGCTCATGTGTCAATGGAATGTTTGGACGGTGA 420
Db 751 GAGAATCTGTACGACGAGGAGAAAGTGCCTGCTCATGTGTCAATGGAATGTTTGGACGGTGA 810
Qy 421 GAATCTTTAGCCGAATTCAGGATTCAGGAGACAGGCAATTCACAGAAAGAGAGCATCC 480
Db 811 GAATCTTTAGCCGAATTCAGGATTCAGGAGACAGGCAATTCACAGAAAGAGAGCATCC 870
Qy 481 GAATCATGAAGAGCATCGGTGAGGCGCATCCAGTATCTGATTCATCAATCAATTCGCCAT 540
Db 871 GAATCATGAAGAGCATCGGTGAGGCGCATCCAGTATCTGATTCATCAATCAATTCGCCAT 930
Qy 541 CGGATGTCAAGCCTGAGAAATCTTTATACACCTCCAAAAGGCCCAACGCCATCTCTGAAA 600
Db 931 CGGATGTCAAGCCTGAGAAATCTTTATACACCTCCAAAAGGCCCAACGCCATCTCTGAAA 990
Qy 601 CTCACTGACTTTGGCTTTGCCAAGGAAACCAACAGGCAAACTCTTTGACCATCTCTTGT 660
Db 991 CTCACTGACTTTGGCTTTGCCAAGGAAACCAACAGGCAAACTCTTTGACCATCTCTTGT 1050
Qy 661 TATACACCGTACTATGTGGTCCAGAAAGTGTGGTCCAGAGAGTATGACAAAGTCTCTGT 720
Db 1051 TATACACCGTACTATGTGGTCCAGAAAGTGTGGTCCAGAGAGTATGACAAAGTCTCTGT 1110
Qy 721 GACATGTGTCCTCGGGTGTGATCATGTATCATCTGCTGTGTGGGTATCCCTTCTCTAC 780
Db 1111 GACATGTGTCCTCGGGTGTGATCATGTATCATCTGCTGTGTGGGTATCCCTTCTCTAC 1170
Qy 781 TCCAAACAGCGCTTCCCATCTCTCCGGGATGAAGACTCGCATCCGAATGGGCGCAGTAT 840
Db 1171 TCCAAACAGCGCTTCCCATCTCTCCGGGATGAAGACTCGCATCCGAATGGGCGCAGTAT 1230
Qy 841 GAATTTCCCAACCCAGAAATGGTCAAGAGTATCAGAGAAAGTGAAGATGCTCATTCGGAAT 900
Db 1231 GAATTTCCCAACCCAGAAATGGTCAAGAGTATCAGAGAAAGTGAAGATGCTCATTCGGAAT 1290
Qy 901 CTGCTGAAAACAGAGCCCAAGAGTATGACCAATCACCAGTGTATGAAACCCCTTGG 960
Db 1291 CTGCTGAAAACAGAGCCCAAGAGTATGACCAATCACCAGTGTATGAAACCCCTTGG 1350
Qy 961 ATCATGCAATCAACAAAGTTCCTCAAACCCCACTGCACACCAAGCGGGTCTTGAAGGAG 1020
Db 1351 ATCATGCAATCAACAAAGTTCCTCAAACCCCACTGCACACCAAGCGGGTCTTGAAGGAG 1410
Qy 1021 GACAAGAGCGGTGGGAGGATGCAAGGAG 1050
Db 1411 GACAAGAGCGGTGGGAGGATGCAAGGAG 1440
```

## RESULT 12

```
US-10-951-406-33
; Sequence 33, Application US/10951406
; Publication No. US20050059630A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; APPLICANT: Chan, Vivien W.
; TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic
; FILE REFERENCE: 16932.002
; CURRENT APPLICATION NUMBER: US/10/951,406
```



[illegible]

RESULT 14

US-10-977-087-33  
 ; Sequence 33, Application US/10977087  
 ; Publication No. US20050130926A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Reinhard, Christoph  
 ; APPLICANT: Jefferson, Anne B.  
 ; APPLICANT: Chan, Vivien W.  
 ; APPLICANT: Kaufmann, Joerg  
 ; APPLICANT: Xin, Hong  
 ; APPLICANT: Kennedy, Giulia C.  
 ; APPLICANT: Khoja, Hamiduddin  
 ; APPLICANT: Shyamala, Venkatakrishna  
 ; TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED IN CANCEROUS CELLS  
 ; TITLE OF INVENTION: AND THEIR METHODS OF USE V  
 ; FILE REFERENCE: 2300-21986  
 ; CURRENT APPLICATION NUMBER: US/10/977,087  
 ; CURRENT FILING DATE: 2004-10-28  
 ; PRIOR APPLICATION NUMBER: 10/081,119  
 ; PRIOR FILING DATE: 2002-02-21  
 ; PRIOR APPLICATION NUMBER: 60/271,254

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Qy 601 CTCACTGACCTTTGGCTTGGCCAGGAACACACAGGCCACAACCTCTTTGACCACTCCTTGT 660
Db 991 CTCACTGACCTTTGGCTTGGCCAGGAACACACAGGCCACAACCTCTTTGACCACTCCTTGT 1050
Qy 661 TATACACCGTACTATGTGGCTCCAGAAAGTGTGGGTCCAGAGAGTATGACAAAGTCCCTGT 720
Db 1051 TATACACCGTACTATGTGGCTCCAGAAAGTGTGGGTCCAGAGAGTATGACAAAGTCCCTGT 1110
Qy 721 GACATGTGGTCCCTGGGTGTCATCATGTACATCTGTGTGTGGGTATCCCCCTTCTAC 780
Db 1111 GACATGTGGTCCCTGGGTGTCATCATGTACATCTGTGTGTGGGTATCCCCCTTCTAC 1170
Qy 781 TCCAACACAGCCCTTGCATCTCTCCGGGCATGAGACTCGCATCCGAATGGGCCAGTAT 840
Db 1171 TCCAACACAGCCCTTGCATCTCTCCGGGCATGAGACTCGCATCCGAATGGGCCAGTAT 1230
Qy 841 GAATTTCCCAACCCAGAAATGTCAGAAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAAT 900
Db 1231 GAATTTCCCAACCCAGAAATGTCAGAAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAAT 1290
Qy 901 CTGCTGAAAAACAGAGCCCAACCCAGAGAAATGACCATCACCGAGTTTATGAACCAACCTTGG 960
Db 1291 CTGCTGAAAAACAGAGCCCAACCCAGAGAAATGACCATCACCGAGTTTATGAACCAACCTTGG 1350
Qy 961 ATCATGCAATCAACAAAGTCCCTCAAAACCCACTGCACACCCAGCCGGTCTTGAAGGAG 1020
Db 1351 ATCATGCAATCAACAAAGTCCCTCAAAACCCACTGCACACCCAGCCGGTCTTGAAGGAG 1410
Qy 1021 GACAAGGAGCGGTGGGAGGATGTCAAGGAG 1050
Db 1411 GACAAGGAGCGGTGGGAGGATGTCAAGGG 1440
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## RESULT 15

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US-10-887-553A-633
; Sequence 633, Application US/10887553A
; Publication No. US20050085436A1
; GENERAL INFORMATION:
; APPLICANT: Garza, Dan
; APPLICANT: Li, Hao
; TITLE OF INVENTION: Method to treat conditions associated
; with insulin signalling dysregulation
; FILE REFERENCE: 4-33262
; CURRENT APPLICATION NUMBER: US/10/887,553A
; CURRENT FILING DATE: 2004-07-08
; PRIOR FILING DATE: 2003-08-07
; NUMBER OF SEQ ID NOS: 1208
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 633
; LENGTH: 3608
; TYPE: DNA
; ORGANISM: human
US-10-887-553A-633
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Query Match 88.0%; Score 1048.4; DB 10; Length 3608;
Best Local Similarity 99.9%; Pred. No. 9e-299;
Matches 1049; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 TCCACAGGCCAGAGCCCGCGGTGCGCGTTCCTCCCGCCCGCGCCCGCGCGCCCGCGCCCGCC 60
Db 299 TCCACAGGCCAGAGCCCGCGGTGCGCGTTCCTCCCGCCCGCGCCCGCGCGCCCGCGCCCG 358
Qy 61 ACCCTGCGCTGCGCAACCCCGCGCGAGCCCGCGCGCCCGCGCGCCCGCGCGAGTTCGCG 120
Db 359 ACCCTGCGCTGCGCAACCCCGCGCGAGCCCGCGCGCCCGCGCGCCCGCGCGAGTTCGCG 418
Qy 121 CAGTTCACGTCAGTCCGGCTCAGATCAAGAAAGCGCCATCATCGATGACTACAAG 180
Db 419 CAGTTCACGTCAGTCCGGCTCAGATCAAGAAAGCGCCATCATCGATGACTACAAG 478
Qy 181 GTCACCAAGCAGGTCCTGGGCTGGGCATCAACCGCAAGTTTTCAGATCTTCAACAAG 240
```

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Db 479 GTCACCAAGCAGGTCCTGGGCTGGGCATCAACCGCAAGTTTTCAGATCTTCAACAAG 538
Qy 241 AGACCCAGAGAGAAATTCGCGCTCAAAATGCTTCAGAGATGCCCCAAGGCCCGCAGGGAG 300
Db 539 AGACCCAGAGAGAAATTCGCGCTCAAAATGCTTCAGAGATGCCCCAAGGCCCGCAGGGAG 598
Qy 301 GTGGAGTGCACGTGGCGGGCTCCCATGTCGCCGCACATCGTACGGATCGTGGATGTGTAC 360
Db 599 GTGGAGTGCACGTGGCGGGCTCCCATGTCGCCGCACATCGTACGGATCGTGGATGTGTAC 658
Qy 361 GAGAACTCTGTACCGAGGAGAAAGTGCCTGCTGATTTGTCATGGAATGTTTGGACGGTGA 420
Db 659 GAGAACTCTGTACCGAGGAGAAAGTGCCTGCTGATTTGTCATGGAATGTTTGGACGGTGA 718
Qy 421 GAACTCTTTAGCCGAATTCAGAGATTCAGAGAGACAGGCATTCACAGAAAGAGACATCC 480
Db 719 GAACTCTTTAGCCGAATTCAGAGATTCAGAGAGACAGGCATTCACAGAAAGAGACATCC 778
Qy 481 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTTCAATCAACATTTGCCCAT 540
Db 779 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTTCAATCAACATTTGCCCAT 838
Qy 541 CGGGATGTCAAGCTTGAGAAATCTTTATACACCTCCAAAAGGCCCAACGCCATCTCTGAAA 600
Db 839 CGGGATGTCAAGCTTGAGAAATCTTTATACACCTCCAAAAGGCCCAACGCCATCTCTGAAA 898
Qy 601 CTCACTGACTTTGGCTTGGTTCAGAGGAAACACACAGGCCAACAATCTTTTGACCACTCTTGT 660
Db 899 CTCACTGACTTTGGCTTGGTTCAGAGGAAACACACAGGCCAACAATCTTTTGACCACTCTTGT 958
Qy 661 TATACACCGTACTATGTGGCTCCAGAGTGTCTGGTCCAGAGAGTATGACAAAGTCTCTGT 720
Db 959 TATACACCGTACTATGTGGCTCCAGAGTGTCTGGTCCAGAGAGTATGACAAAGTCTCTGT 1018
Qy 721 GACATGTGGTCCCTGGGTGTCATCATGTATCATCTGTGTGGGTATCCCCCTTCTAC 780
Db 1019 GACATGTGGTCCCTGGGTGTCATCATGTATCATCTGTGTGGGTATCCCCCTTCTAC 1078
Qy 781 TCCAAACACAGGCCCTTGCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 840
Db 1079 TCCAAACACAGGCCCTTGCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 1138
Qy 841 GAATTTCCCAACCCAGAAATGTCAGAGAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT 900
Db 1139 GAATTTCCCAACCCAGAAATGTCAGAGAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT 1198
Qy 901 CTGCTGAAAAACAGAGCCCAACCCAGAGAAATGACCATCAACCGAGTTTATGAACCAACCTTGG 960
Db 1199 CTGCTGAAAAACAGAGCCCAACCCAGAGAAATGACCATCAACCGAGTTTATGAACCAACCTTGG 1258
Qy 961 ATCATGCAATCAACAAAGTTCCTCAACCCCACTGCACACCCAGCCGGTCTTGAAGGAG 1020
Db 1259 ATCATGCAATCAACAAAGTTCCTCAACCCCACTGCACACCCAGCCGGTCTTGAAGGAG 1318
Qy 1021 GACAAGGAGCGGTGGGAGGATGTCAAGGAG 1050
Db 1319 GACAAGGAGCGGTGGGAGGATGTCAAGGG 1348
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Search completed: June 19, 2006, 17:13:06  
Job time : 1546 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein\_search, using sw model

Run on: June 19, 2006, 08:51:16 ; Search time 199 Seconds  
(without alignments)  
909.838 Million cell updates/sec

Title: US-10-469-221-2

Perfect score: 2106

Sequence: 1 SQGSPVPVPPAPAPPQP.....PLLLKRRKARALEAALAH 396

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A\_Geneseq\_8:\*

- 1: Geneseq1980s:\*
- 2: Geneseq1990s:\*
- 3: Geneseq2000s:\*
- 4: Geneseq2001s:\*
- 5: Geneseq2002s:\*
- 6: Geneseq2003as:\*
- 7: Geneseq2003bs:\*
- 8: Geneseq2004s:\*
- 9: Geneseq2005s:\*
- 10: Geneseq2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2106	100.0	396	6 AAE29898	Human tru
2	2106	100.0	400	6 AAE29899	Human ful
3	2106	100.0	400	7 ADC15042	Mitogen a
4	2106	100.0	400	7 ADE58649	Human Pro
5	2106	100.0	400	7 ADN02271	Human MK-
6	2106	100.0	400	8 ADM61583	Human nat
7	2097	99.6	400	8 ADM36340	Human MK2
8	2097	99.6	400	9 ADX06660	Cyclin-de
9	1921	91.2	385	7 ADE60496	Rat Prote
10	1921	91.2	385	7 ADD47657	Rat Prote
11	1886	89.6	378	8 ABM82670	Human dia
12	1882	89.4	370	5 ABP54949	Human MAP
13	1882	89.4	370	7 ABU61622	Human can
14	1882	89.4	370	8 ADM36338	Human MK2
15	1882	89.4	370	8 ADP87579	Human NOV
16	1882	89.4	370	9 ADX06658	Cyclin-de
17	1882	89.4	370	9 ADY86798	Human MAP
18	1882	89.4	370	9 AEA89440	Human MAP
19	1882	89.4	375	8 ADP87585	Human NOV
20	1870	88.8	370	8 ADP87583	Human NOV
21	1870	88.8	370	8 ADP87587	Human NOV
22	1828	86.8	357	9 ADY85543	Catalytic
23	1803	85.6	338	8 ADP87589	Human NOV

24	1729	82.1	327	7	ADN02272	Human MK-
25	1729	82.1	434	6	ABR83629	SUMO-MPAK
26	1716	81.5	326	8	ADN61586	Human MAP
27	1596	75.8	324	6	ABR41296	Human DIT
28	1552	73.7	294	8	ADP87591	Human NOV
29	1552	73.7	294	8	ADP87581	Human NOV
30	1391	66.0	382	2	AAW31910	Human MAP
31	1391	66.0	382	7	ADC15043	Mitogen a
32	1391	66.0	382	7	ADD14163	Human src
33	1391	66.0	382	7	ADE60498	Human Pro
34	1391	66.0	382	7	ADD47659	Human Pro
35	1391	66.0	382	7	ADN95701	Human BEC
36	1391	66.0	382	8	ADN03900	Antipsori
37	1391	66.0	382	8	ADN61584	Human MAP
38	1391	66.0	382	8	ADO52466	Human BRC
39	1391	66.0	382	8	ABM80460	Tumour-as
40	1391	66.0	382	9	AEE19659	Human MAP
41	1391	66.0	383	7	ADD46033	Human Pro
42	1381	65.6	382	9	AEE19663	Human MAP
43	1379	65.5	382	9	AEE19665	Human MAP
44	1261.5	59.9	355	8	ABM83772	Human dia
45	1261.5	59.9	355	8	ABM83774	Human dia

## ALIGNMENTS

RESULT 1

AAE29898

ID AAE29898 standard; protein; 396 AA.

XX

AC AAE29898;

XX

DT 24-MAR-2003 (first entry)

XX

DE Human truncated MAPKAP-2 kinase, tdnMAPKAP-2.

XX

KW Human; mitogen-activated protein kinase activating protein kinase-2;  
MAPKAP-2 kinase; signal transduction; cell proliferative disorder;  
immune system disorder; inflammation; arthritis; immunomodulator;  
cytostatic; gene therapy; enzyme.

XX

OS Homo sapiens.

XX

PN WO200290524-A2.

XX

PD 14-NOV-2002.

XX

PF 25-FEB-2002; 2002WO-US005670.

XX

PR 28-FEB-2001; 2001US-0272360P.

XX

PA (MERI ) MERCK & CO INC.

XX

PI Lograsso P, Hawkins J, Lisnock JM;

XX

DR WPI; 2003-111970/10.

XX

DR N-PSDB; AAD50036.

XX

PT New isolated nucleic acid molecule encoding a human mitogen-activated

XX

PT protein kinase activating protein kinase-2 (MAPKAP-2), useful for

XX

XX treating immune-system related disorders, inflammation and arthritis.

PS Claim 11; Fig 2; 150pp; English.

XX

CC The invention relates to an isolated nucleic acid molecule comprising a  
sequence of nucleotides that encode a human mitogen-activated protein  
kinase activating protein kinase-2 (MAPKAP-2 kinase) and a coding region  
that encodes a splice variant of a MAPKAP-2 kinase. The invention is  
especially useful in regulating signal transduction in a cell and in  
diagnosing or treating MAPKAP-2-mediated disorders eg. cell proliferative  
disorders, immune system disorders, inflammation, arthritis. The nucleic  
acid and the polypeptide may also be used in screening assays, predictive

CC medicine, diagnostic or prognostic assays, chromosome mapping, tissue  
 CC typing, pharmacogenomics and in monitoring clinical trials. The invention  
 CC is useful in gene therapy. The present sequence is human truncated MAPKAP  
 CC -2 kinase, tdnMAPKAP-2  
 XX  
 SQ Sequence 396 AA;  
 Query Match 100.0%; Score 2106; DB 6; Length 396;  
 Best Local Similarity 100.0%; Pred. No. 2e-161;  
 Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SQGSPVPVPAPAPPQPTPALPHPPAQPFPQFHVKSGLQIKKNAIIDDYK 60  
 DB 1 SQGSPVPVPAPAPPQPTPALPHPPAQPFPQFHVKSGLQIKKNAIIDDYK 60  
 QY 61 VTSQVLGLGKINGKVLQIFNKRTQEKFKALQDCPKARREVELHWRASQCPHIVRVDVY 120  
 DB 61 VTSQVLGLGKINGKVLQIFNKRTQEKFKALQDCPKARREVELHWRASQCPHIVRVDVY 120  
 QY 121 ENLYAGRKCLLIWECLDGGELFSRIQDRGDOAFTEREASEIMKSGEAIQYLHSINIAH 180  
 DB 121 ENLYAGRKCLLIWECLDGGELFSRIQDRGDOAFTEREASEIMKSGEAIQYLHSINIAH 180  
 QY 181 RDVKNPENVLTSKRPNAILKLTDFGFAKETTSHNSLTTPCYTPYYVAPEVLGPEKDYKSC 240  
 DB 181 RDVKNPENVLTSKRPNAILKLTDFGFAKETTSHNSLTTPCYTPYYVAPEVLGPEKDYKSC 240  
 QY 241 DMWSLGVIMYILLCGYPPFYSNHGLAISPGMKTRIRMGQYEFNPNPSEVSEVKMLRN 300  
 DB 241 DMWSLGVIMYILLCGYPPFYSNHGLAISPGMKTRIRMGQYEFNPNPSEVSEVKMLRN 300  
 QY 301 LLKTEPTQRMWITTEFNNHPIMQSTKVPTPLHTSRVLKEDKRWEDVKEEMTSALATMR 360  
 DB 301 LLKTEPTQRMWITTEFNNHPIMQSTKVPTPLHTSRVLKEDKRWEDVKEEMTSALATMR 360  
 QY 361 VDYEQIKIKKIEDASNPILLKRRKKARALEAALAH 396  
 DB 361 VDYEQIKIKKIEDASNPILLKRRKKARALEAALAH 396  
 RESULT 2  
 AAEE29899  
 ID AAEE29899 standard; protein; 400 AA.  
 XX  
 AC AAEE29899;  
 XX  
 DT 24-MAR-2003 (first entry)  
 XX  
 DE Human full length MAPKAP-2 kinase, fldnaMAPKAP-2.  
 XX  
 KW Human; mitogen-activated protein kinase activating protein kinase-2;  
 KW MAPKAP-2 kinase; signal transduction; cell proliferative disorder;  
 KW immune system disorder; inflammation; arthritis; immunomodulator;  
 KW cytostatic; gene therapy; enzyme.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200290524-A2.  
 XX  
 PD 14-NOV-2002.  
 XX  
 PF 25-FEB-2002; 2002WO-US005670.  
 XX  
 PR 28-FEB-2001; 2001US-0272260P.  
 XX  
 PA (MERI ) MERCK & CO INC.  
 XX  
 PI Lograsso P, Hawkins J, Lisnock JM;  
 XX  
 DR WPI; 2003-111970/10.  
 DR N-PSDB; AP050037.  
 XX  
 PT New isolated nucleic acid molecule encoding a human mitogen-activated

PT protein kinase activating protein kinase-2 (MAPKAP-2), useful for  
 PT treating immune-system related disorders, inflammation and arthritis.  
 XX  
 PS Claim 66; Fig 4; 150pp; English.  
 XX  
 CC The invention relates to an isolated nucleic acid molecule comprising a  
 CC sequence of nucleotides that encode a human mitogen-activated protein  
 CC kinase activating protein kinase-2 (MAPKAP-2 kinase) and a coding region  
 CC that encodes a splice variant of a MAPKAP-2 kinase. The invention is  
 CC especially useful in regulating signal transduction in a cell and in  
 CC diagnosing or treating MAPKAP-2-mediated disorders eg. cell proliferative  
 CC disorders, immune system disorders, inflammation, arthritis. The nucleic  
 CC acid and the polypeptide may also be used in screening assays, predictive  
 CC medicine, diagnostic or prognostic assays, chromosome mapping, tissue  
 CC typing, pharmacogenomics and in monitoring clinical trials. The invention  
 CC is useful in gene therapy. The present sequence is human full length  
 CC MAPKAP-2 kinase, fldnaMAPKAP-2  
 XX  
 SQ Sequence 400 AA;  
 Query Match 100.0%; Score 2106; DB 6; Length 400;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-161;  
 Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SQGSPVPVPAPAPPQPTPALPHPPAQPFPQFHVKSGLQIKKNAIIDDYK 60  
 DB 5 SQGSPVPVPAPAPPQPTPALPHPPAQPFPQFHVKSGLQIKKNAIIDDYK 64  
 QY 61 VTSQVLGLGKINGKVLQIFNKRTQEKFKALQDCPKARREVELHWRASQCPHIVRVDVY 120  
 DB 65 VTSQVLGLGKINGKVLQIFNKRTQEKFKALQDCPKARREVELHWRASQCPHIVRVDVY 124  
 QY 121 ENLYAGRKCLLIWECLDGGELFSRIQDRGDOAFTEREASEIMKSGEAIQYLHSINIAH 180  
 DB 125 ENLYAGRKCLLIWECLDGGELFSRIQDRGDOAFTEREASEIMKSGEAIQYLHSINIAH 184  
 QY 181 RDVKNPENVLTSKRPNAILKLTDFGFAKETTSHNSLTTPCYTPYYVAPEVLGPEKDYKSC 240  
 DB 185 RDVKNPENVLTSKRPNAILKLTDFGFAKETTSHNSLTTPCYTPYYVAPEVLGPEKDYKSC 244  
 QY 241 DMWSLGVIMYILLCGYPPFYSNHGLAISPGMKTRIRMGQYEFNPNPSEVSEVKMLRN 300  
 DB 245 DMWSLGVIMYILLCGYPPFYSNHGLAISPGMKTRIRMGQYEFNPNPSEVSEVKMLRN 304  
 QY 301 LLKTEPTQRMWITTEFNNHPIMQSTKVPTPLHTSRVLKEDKRWEDVKEEMTSALATMR 360  
 DB 305 LLKTEPTQRMWITTEFNNHPIMQSTKVPTPLHTSRVLKEDKRWEDVKEEMTSALATMR 364  
 QY 361 VDYEQIKIKKIEDASNPILLKRRKKARALEAALAH 396  
 DB 365 VDYEQIKIKKIEDASNPILLKRRKKARALEAALAH 400  
 RESULT 3  
 ADC15042  
 ID ADC15042 standard; protein; 400 AA.  
 XX  
 AC ADC15042;  
 XX  
 DT 18-DEC-2003 (first entry)  
 XX  
 DE Mitogen activated protein kinase activated protein kinase 2 (MAPKAPK2).  
 XX  
 KW Mitogen activated protein kinase activated protein kinase 2; MAPKAPK2;  
 KW crystal structure; three dimensional structure; ATP binding pocket;  
 KW substrate binding pocket; nuclear export signal motif;  
 KW MAP kinase signal transduction pathway; cellular stress;  
 KW bacterial lipopolysaccharide; proinflammatory cytokine; TNF-alpha;  
 KW tumour necrosis factor-alpha; drug screening; rational drug design;  
 KW protein co-ordinate data; enzyme.  
 XX  
 OS Unidentified.  
 XX



PH Key Location/Qualifiers  
 FT Binding-site 77..78 /note= "These residues are part of the ATP binding pocket"  
 FT Binding-site 80 /note= "This residue is part of the ATP binding pocket"  
 FT Binding-site 91..93 /note= "These residues are part of the ATP binding pocket"  
 FT Binding-site 104 /note= "This residue is part of the ATP binding pocket"  
 FT Binding-site 108 /note= "This residue is part of the ATP binding pocket"  
 FT Binding-site 118 /note= "This residue is part of the ATP binding pocket"  
 FT Binding-site 136 /note= "This residue is part of the ATP binding pocket"  
 FT Binding-site 138..141 /note= "These residues are part of the ATP binding pocket"  
 FT Binding-site 144..145 /note= "These residues are part of the ATP binding pocket"  
 FT Active-site 147 /note= "This residue is part of the substrate binding pocket"  
 FT Active-site 151 /note= "This residue is part of the substrate binding pocket"  
 FT Active-site 158 /note= "This residue is part of the substrate binding pocket"  
 FT Active-site 160..161 /note= "These residues are part of the substrate binding pocket"  
 FT Active-site 164 /note= "This residue is part of the substrate binding pocket"  
 FT Active-site 185..186 /note= "These residues are part of the substrate binding pocket"  
 FT Active-site 188..190 /note= "These residues are part of the substrate binding pocket"  
 FT Binding-site 190..191 /note= "These residues are part of the ATP binding pocket"  
 FT Binding-site 193 /note= "This residue is part of the ATP binding pocket"  
 FT Binding-site 206..207 /note= "These residues are part of the ATP binding pocket"  
 FT Active-site 210 /note= "This residue is part of the substrate binding pocket"  
 FT Region 217..235 /note= "Activation loop"  
 FT Active-site 240 /note= "This residue is part of the substrate binding pocket"  
 FT Active-site 244 /note= "This residue is part of the substrate binding pocket"  
 FT Active-site 247..248 /note= "These residues are part of the substrate binding pocket"  
 FT Active-site 251..252 /note= "These residues are part of the substrate binding pocket"  
 FT Active-site 256..257 /note= "These residues are part of the substrate binding pocket"  
 FT Active-site 259..261 /note= "These residues are part of the substrate binding pocket"

FT /note= "These residues are part of the substrate binding pocket"  
 FT 328..400 /note= C-terminal regulatory domain  
 FT Modified-site 334 /note= "Thr is optionally O-phosphorylated. This is a major regulatory phosphorylation site"  
 FT Modified-site 338 /note= "Thr is optionally O-phosphorylated. This is an auto-phosphorylation site"  
 FT Region 345..368 /note= "Nuclear export signal (NES) motif"  
 FT Region 373..389 /note= "Nuclear localisation signal motif"  
 FT Binding-site 385..389 /note= "Docking site for activator protein p38"  
 XX WO2003048340-A2.  
 PN 12-JUN-2003.  
 XX 05-DEC-2002; 2002WO-US039070.  
 XX 05-DEC-2001; 2001US-0337513P.  
 PA (VERT-) VERTEX PHARM INC.  
 XX Meng W, Swenson L;  
 XX WPI; 2003-482712/45.  
 DR Crystalline molecule comprising an ATP binding pocket, substrate binding pocket or nuclear export signal binding pocket of mitogen activated protein kinase-2, useful for designing binding compounds.  
 XX Claim 1; SEQ ID NO 1; 172pp; English.  
 XX The invention relates to the crystal structure of mitogen activated protein kinase activated protein kinase 2 (MAPKAPK2), its homologues and molecular complexes comprising MAPKAPK2. The MAPKAPK2 crystal structure comprises the ATP binding pocket, the substrate binding pocket and the nuclear export signal (NES) motif. MAPKAPK2 is an intracellular component of the MAP kinase signal transduction pathway that is triggered in response to cellular stresses such as heat or osmotic shock, bacterial lipopolysaccharide, proinflammatory cytokines and TNF-alpha (tumour necrosis factor-alpha). It is located in the nucleus of unstimulated cells and rapidly moves to the cytoplasm on activation by the kinases p38/p40/RK. While in the nucleus, MAPKAPK2 contributes to the phosphorylation of CREB (cAMP response element-binding protein), and is also responsible for phosphorylating serum response factor and the transcription factor E47. In the cytoplasm, MAPKAPK2 phosphorylates the small heat shock protein HSP25/HSP27, lymphocyte specific protein (LSP1), glycogen synthase, tyrosine hydroxylase (the rate-limiting enzyme in catecholamine synthesis) and 5-lipoxygenase, a key enzyme in leukotriene biosynthesis. Mice which lack MAPKAPK2 show increased stress resistance and survive bacterial LPS-induced endotoxic shock due to a 90% reduction in the production of TNF-alpha. The crystal structure of MAPKAPK2 may be used to evaluate the ability of a chemical entity to interact with binding pockets or other key domains of MAPKAPK2, and in rational drug design. MAPKAPK2-specific agonists and antagonists identified using the crystal structure may be used in the treatment of disorders related to MAPKAPK2. The present sequence represents MAPKAPK2.  
 XX Sequence 400 AA;  
 SQ Query Match 100.0%; Score 2106; DB 7; Length 400;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-161;  
 Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 SQGSPVPVPAPAPPQPTPALPHPPAQQPQQFQFHVKSLQIKKNAIIDYK 60  
 Db 5 SQGSPVPVPAPAPPQPTPALPHPPAQQPQQFQFHVKSLQIKKNAIIDYK 64

QY 61 VTSQVLGLGKNGKVLQIFNKRTOEKFKALQMLQDCPKARRVELHWRASQCPHIVRVDVY 120  
 DB 65 VTSQVLGLGKNGKVLQIFNKRTOEKFKALQMLQDCPKARRVELHWRASQCPHIVRVDVY 124  
 QY 121 ENLYAGRKCLLIWECLDGGELEFSRIQDRGDOAFTEREASEIMKSGEAIQYLHSINIAH 180  
 DB 125 ENLYAGRKCLLIWECLDGGELEFSRIQDRGDOAFTEREASEIMKSGEAIQYLHSINIAH 184  
 QY 181 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSNLSLTPCYTPYYVAPEVLGPEKYDKSC 240  
 DB 185 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSNLSLTPCYTPYYVAPEVLGPEKYDKSC 244  
 QY 241 DMWSLGVIMVILLCGYPPFYNSHGLAISPGMKTRIRMGQYEFNPNPSEVSEEVKMLIRN 300  
 DB 245 DMWSLGVIMVILLCGYPPFYNSHGLAISPGMKTRIRMGQYEFNPNPSEVSEEVKMLIRN 304  
 QY 301 LLKTEPTQRTMITTEFMNHPIMQSTKVPQTPPLHTSRVLKEDKRWEDVKEMTSALATMR 360  
 DB 305 LLKTEPTQRTMITTEFMNHPIMQSTKVPQTPPLHTSRVLKEDKRWEDVKEMTSALATMR 364  
 QY 361 VDYEQIKIKKIEDASNPILLKRRKKARALEAALAH 396  
 DB 365 VDYEQIKIKKIEDASNPILLKRRKKARALEAALAH 400

RESULT 4  
 ADE58649  
 ID ADE58649 standard; protein; 400 AA.  
 XX AC ADE58649;  
 XX DT 29-JAN-2004 (first entry)  
 XX DE Human Protein P49137, SEQ ID NO 4525.  
 XX KW Human; pain; neuronal tissue; gene therapy;  
 KW spinal segmental nerve injury; chronic constriction injury; CCI;  
 KW spared nerve injury; SNI; Chung.  
 XX OS Homo sapiens.  
 XX PN W02003016475-A2.  
 XX PD 27-FEB-2003.  
 XX PF 14-AUG-2002; 2002WO-US025765.  
 XX PR 14-AUG-2001; 2001US-0312147P.  
 PR 01-NOV-2001; 2001US-0346382P.  
 PR 26-NOV-2001; 2001US-0333347P.  
 XX (GEHO ) GEN HOSPITAL CORP.  
 PA (FARB ) BAYER AG.  
 XX PI Woolf C, D'urso D, Befort K, Costigan M;  
 XX WPI; 2003-268312/26.  
 DR GENBANK; P49137.  
 XX PT New composition comprising two or more isolated polypeptides, useful for  
 PT preparing a medicament for treating pain in an animal.  
 XX PS Claim 1; Page; 1017pp; English.  
 XX CC The invention discloses a composition comprising two or more isolated rat  
 CC or human polynucleotides or a polynucleotide which represents a fragment,  
 CC derivative or allelic variation of the nucleic acid sequence. Also  
 CC claimed are a vector comprising the novel polynucleotide, a host cell  
 CC comprising the vector, a method for identifying a nucleotide sequence  
 CC which is differentially regulated in an animal subjected to pain and a  
 CC kit to perform the method, an array, a method for identifying an agent  
 CC that increases or decreases the expression of the polynucleotide sequence

CC that is differentially expressed in neuronal tissue of a first animal  
 CC subjected to pain, a method for identifying a compound which regulates  
 CC the expression of a polynucleotide sequence which is differentially  
 CC expressed in an animal subjected to pain, a method for identifying a  
 CC compound that regulates the activity of one or more of the  
 CC polynucleotides, a method for producing a pharmaceutical composition, a  
 CC method for identifying a compound or small molecule that regulates the  
 CC activity in an animal of one or more of the polypeptides given in the  
 CC specification, a method for identifying a compound useful in treating  
 CC pain and a pharmaceutical composition comprising the one or more  
 CC polypeptides or their antibodies. The polynucleotide or the compound that  
 CC modulates its activity is useful for preparing a medicament for treating  
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
 CC therapy). The sequence presented is a human protein (shown in Table 2 of  
 CC the specification) which is differentially expressed during pain. Note:  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic form directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.  
 XX Sequence 400 AA;  
 XX Query Match 100.0%; Score 2106; DB 7; Length 400;  
 XX Best Local Similarity 100.0%; Pred. No. 2.1e-161;  
 XX Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SQQSPPVPPAPAPPPQPPPTPALPHPPAQQPPPPPPQPPQFHVKSLQIKKNAIDDYK 60  
 DB 5 SQQSPPVPPAPAPPPQPPPTPALPHPPAQQPPPPPPQPPQFHVKSLQIKKNAIDDYK 64  
 QY 61 VTSQVLGLGKNGKVLQIFNKRTOEKFKALQMLQDCPKARRVELHWRASQCPHIVRVDVY 120  
 DB 65 VTSQVLGLGKNGKVLQIFNKRTOEKFKALQMLQDCPKARRVELHWRASQCPHIVRVDVY 124  
 QY 121 ENLYAGRKCLLIWECLDGGELEFSRIQDRGDOAFTEREASEIMKSGEAIQYLHSINIAH 180  
 DB 125 ENLYAGRKCLLIWECLDGGELEFSRIQDRGDOAFTEREASEIMKSGEAIQYLHSINIAH 184  
 QY 181 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSNLSLTPCYTPYYVAPEVLGPEKYDKSC 240  
 DB 185 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSNLSLTPCYTPYYVAPEVLGPEKYDKSC 244  
 QY 241 DMWSLGVIMVILLCGYPPFYNSHGLAISPGMKTRIRMGQYEFNPNPSEVSEEVKMLIRN 300  
 DB 245 DMWSLGVIMVILLCGYPPFYNSHGLAISPGMKTRIRMGQYEFNPNPSEVSEEVKMLIRN 304  
 QY 301 LLKTEPTQRTMITTEFMNHPIMQSTKVPQTPPLHTSRVLKEDKRWEDVKEMTSALATMR 360  
 DB 305 LLKTEPTQRTMITTEFMNHPIMQSTKVPQTPPLHTSRVLKEDKRWEDVKEMTSALATMR 364  
 QY 361 VDYEQIKIKKIEDASNPILLKRRKKARALEAALAH 396  
 DB 365 VDYEQIKIKKIEDASNPILLKRRKKARALEAALAH 400

RESULT 5  
 ADN02271  
 ID ADN02271 standard; protein; 400 AA.  
 XX AC ADN02271;  
 XX DT 17-JUN-2004 (first entry)  
 XX DE Human MK-2 amino acid sequence, seq id 1.  
 XX KW Antiinflammatory; MK-2 inhibitor; crystalline MK-2;  
 KW mitogen-activated protein kinase-activated protein kinase-2; enzyme;  
 KW inflammation; human; protein co-ordinate data.  
 XX OS Homo sapiens.  
 XX PN W02003076333-A2.  
 XX

PD 18-SEP-2003.  
XX  
XX  
PF 06-MAR-2003; 2003WO-US006849.  
XX  
XX 07-MAR-2002; 2002US-0362380P.  
PR 04-APR-2002; 2002US-00116649.  
XX  
XX (PHAA ) PHARMACIA CORP.  
XX  
XX Kurumbail RG, Pawlitz JL, Stegeman RA, Stallings WC, Shieh H;  
PI Mourey RJ, Bollen SL, Broadus RM;  
XX  
XX WPI; 2003-767406/72.  
XX  
XX New crystalline mitogen-activated protein kinase-activated protein kinase  
PT -2, useful for designing and identifying inhibitors as potential  
PT antiinflammatory agents.  
XX  
XX Disclosure; SEQ ID NO 1; 135pp; English.  
XX  
XX The invention relates to crystalline MK-2 (mitogen-activated protein  
CC kinase-activated protein kinase-2). Further disclosed is a human MK-2  
CC construct, and a crystalline composition comprising MK-2 in a co-complex  
CC with another compound (I). Also disclosed is a computer-assisted method  
CC for designing an inhibitor of MK-2 activity de novo. Protein co-ordinate  
CC data is given in the specification. Crystalline MK-2 is used to produce  
CC structural co-ordinates and these are used for identification and design  
CC of inhibitors of MK-2, potentially useful for treating inflammation. The  
CC current sequence represents the human MK-2 protein.  
XX  
XX Sequence 400 AA;  
SQ  
Query Match 100.0%; Score 2106; DB 7; Length 400;  
Best Local Similarity 100.0%; Pred. No. 2.1e-161; Indels 0; Gaps 0;  
Matches 396; Conservative 0; Mismatches 0;  
Qy 1 SQGSPVPFPAPAPPQPPPTPALPHPPAQPQPPPPQFPQFHVKSGLIQKNAIIDYK 60  
Db 5 SQGSPVPFPAPAPPQPPPTPALPHPPAQPQPPPPQFPQFHVKSGLIQKNAIIDYK 64  
Qy 61 VTSQVLGLGKINGKVLQIFNKRTOBKFPALKMLQDCPKARREVELHWRASQCPHIVRVDVY 120  
Db 65 VTSQVLGLGKINGKVLQIFNKRTOBKFPALKMLQDCPKARREVELHWRASQCPHIVRVDVY 124  
Qy 121 ENLYAGRKCLLIYMECLDGGELFSRIQDRGDOAFTEREASEIMKSGEATQYLHSINIAH 180  
Db 125 ENLYAGRKCLLIYMECLDGGELFSRIQDRGDOAFTEREASEIMKSGEATQYLHSINIAH 184  
Qy 181 RDVKPENLLYTSKRPNAIKLITDFGFAKETTSNLSLTPCYTPYYVAPEVLGPEKYDKSC 240  
Db 185 RDVKPENLLYTSKRPNAIKLITDFGFAKETTSNLSLTPCYTPYYVAPEVLGPEKYDKSC 244  
Qy 241 DMWSLGVIMYLLCGYPPFPYSNHLAISPGMKTRIRMGQYEFPPNPEVSEVVKMLRN 300  
Db 245 DMWSLGVIMYLLCGYPPFPYSNHLAISPGMKTRIRMGQYEFPPNPEVSEVVKMLRN 304  
Qy 301 LLKTEPTQRTMITFNMHPIMQSTKVPOTPLHTSRVLKEDKRWEDVKEMTSALATMR 360  
Db 305 LLKTEPTQRTMITFNMHPIMQSTKVPOTPLHTSRVLKEDKRWEDVKEMTSALATMR 364  
Qy 361 VDYEQIKKIEDASNPILLKRRKKARALEAAALAH 396  
Db 365 VDYEQIKKIEDASNPILLKRRKKARALEAAALAH 400  
RESULT 6  
ADN61583  
ID ADN61583 standard; protein; 400 AA.  
XX  
XX AC ADN61583;  
XX  
XX 29-JUL-2004 (first entry)  
XX

DE  
XX  
XX Human native MAP kinase activated protein kinase 2 (MK2).  
KW Crystal structure; human;  
KW mitogen activated protein kinase activated protein kinase 2;  
KW MAP kinase activated protein kinase 2; MK2; drug design; crystallography;  
KW inflammatory disease; antiinflammatory; protein co-ordinate data; enzyme.  
XX  
OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH 41.364  
FT /note="Region specifically claimed in Claim 2"  
XX  
XX US2004091872-A1.  
XX  
XX 13-MAY-2004.  
PD  
XX 13-NOV-2002; 2002US-00294027.  
PF  
XX 13-NOV-2002; 2002US-00294027.  
PR  
XX (PARR/) PARRIS K D.  
XX (UNDE/) UNDERWOOD K W.  
PA (STAH/) STAHL M L.  
PA (MOSY/) MOSYAK L.  
PA (SVEN/) SVENSON K.  
PA (SHAN/) SHANE T.  
PA (TAYL/) TAYLOR M L.  
XX  
XX Parris KD, Underwood KW, Stahl ML, Mosyak L, Svenson K, Shane T;  
PI Taylor ML;  
XX  
XX WPI; 2004-410434/38.  
DR  
XX Novel isolated mitogen activated protein kinase activated protein kinase  
PT polypeptides, useful as therapeutic agents in treating inflammatory based  
PT diseases.  
XX  
XX Claim 2; SEQ ID NO 1; 272pp; English.  
PS  
XX The present invention relates to the crystal structures of human mitogen  
CC activated protein (MAP) kinase activated protein kinase 2 (MK2), and the  
CC use of these structures in drug design. Also disclosed are the  
CC polynucleotide sequence encoding MK2, a vector comprising the  
CC polynucleotide, a transformed host cell transfected or infected with the  
CC vector, and a method of producing crystallised MK2. The crystallised MK2  
CC is useful as a therapeutic agent in treating inflammatory based diseases.  
CC The present sequence represents human MK2.  
XX  
XX Sequence 400 AA;  
SQ  
Query Match 100.0%; Score 2106; DB 8; Length 400;  
Best Local Similarity 100.0%; Pred. No. 2.1e-161; Indels 0; Gaps 0;  
Matches 396; Conservative 0; Mismatches 0;  
Qy 1 SQGSPVPFPAPAPPQPPPTPALPHPPAQPQPPPPQFPQFHVKSGLIQKNAIIDYK 60  
Db 5 SQGSPVPFPAPAPPQPPPTPALPHPPAQPQPPPPQFPQFHVKSGLIQKNAIIDYK 64  
Qy 61 VTSQVLGLGKINGKVLQIFNKRTOBKFPALKMLQDCPKARREVELHWRASQCPHIVRVDVY 120  
Db 65 VTSQVLGLGKINGKVLQIFNKRTOBKFPALKMLQDCPKARREVELHWRASQCPHIVRVDVY 124  
Qy 121 ENLYAGRKCLLIYMECLDGGELFSRIQDRGDOAFTEREASEIMKSGEATQYLHSINIAH 180  
Db 125 ENLYAGRKCLLIYMECLDGGELFSRIQDRGDOAFTEREASEIMKSGEATQYLHSINIAH 184  
Qy 181 RDVKPENLLYTSKRPNAIKLITDFGFAKETTSNLSLTPCYTPYYVAPEVLGPEKYDKSC 240  
Db 185 RDVKPENLLYTSKRPNAIKLITDFGFAKETTSNLSLTPCYTPYYVAPEVLGPEKYDKSC 244  
Qy 241 DMWSLGVIMYLLCGYPPFPYSNHLAISPGMKTRIRMGQYEFPPNPEVSEVVKMLRN 300  
XX

Db 245 DMSLGVIMVILLCGVPPFVSNHGLAISPGMKTRIRMGQYEFNPNPSEVSEVKMLRN 304  
Qy 301 LLKTEPTQRMITTEFMNHPIMOSTKVPQTPPLHTSRVLKEDKERWEDVKEEMTSALATMR 360  
Db 305 LLKTEPTQRMITTEFMNHPIMOSTKVPQTPPLHTSRVLKEDKERWEDVKEEMTSALATMR 364  
Qy 361 VDYEQIKIKKIEDASNPILLKRRKKARALEAALAH 396  
Db 365 VDYEQIKIKKIEDASNPILLKRRKKARALEAALAH 400

RESULT 7  
ADM36340  
ID ADM36340 standard; protein; 400 AA.  
XX  
XX ADM36340;  
XX  
DT 03-JUN-2004 (first entry)  
XX  
XX Human MK2 variant 2 protein SEQ ID NO:4.  
XX  
XX ischaemic injury;  
KW mitogen-activated protein kinase-activated protein kinase 2; MK2;  
KW vasotrophic; cerebroprotective; cardiant; hypotensive;  
KW antiarteriosclerotic; thrombolytic; neuroprotective; cardiovascular;  
KW antianginal; antiarrhythmic; MK2 antagonist; cerebral ischaemia;  
KW ischaemia; vascular occlusion; cerebral infarction; stroke;  
KW cerebral vascular disease; myocardial infarction;  
KW coronary artery disease; congestive heart failure; cardiac arrhythmia;  
KW unstable angina; high blood pressure; claudication;  
KW peripheral occlusive arterial disease; atherosclerosis;  
KW thrombotic condition; thromboembolic condition; CNS disorder; human;  
KW MK2 variant 2; chromosome 1q32.  
XX  
OS Homo sapiens.  
XX  
XX W02004017909-A2.  
XX  
XX 04-MAR-2004.  
XX  
XX 21-AUG-2003; 2003WO-US026337.  
XX  
XX 23-AUG-2002; 2002US-0405586P.  
XX  
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.  
XX  
XX Wang X, Schieven G, Feuerstein GZ;  
XX  
XX WPI; 2004-226726/21.  
XX  
XX N-PSDB; ADM36339.  
XX  
XX Reducing or treating ischemic injury, comprises administering an  
PT inhibitor of mitogen-activated protein kinase-activated protein kinase 2  
PT (MK2) activity or expression.  
XX  
XX Disclosure; SEQ ID NO 4; 39pp; English.  
XX

The present invention describes a method for reducing ischaemic injury in a mammal, which comprises administering a compound that reduces the activity of mitogen-activated protein kinase-activated protein kinase 2 (MK2) or that inhibits MK2 expression. Also described: (1) identifying a compound which inhibits MK2 expression in a cell, or which modulates MK2 activity; (2) compounds identified by the method above; and (3) treating ischaemic injury by administering to a patient a compound above, or an MK2 modulator. The compound has vasotropic, cerebroprotective, cardiant, hypotensive, antiarteriosclerotic, thrombolytic, neuroprotective, cardiovascular, antianginal and antiarrhythmic activities, and can be used as an MK2 antagonist. The method is useful reducing or treating ischaemic injury, particularly cerebral ischaemia. Compounds identified by the method are useful for treating ischaemia, (e.g. ischaemia resulting from vascular occlusion, cerebral infarction, stroke, and related cerebral vascular diseases), myocardial infarction, coronary artery disease, congestive heart failure, cardiac arrhythmias, unstable

CC angina, high blood pressure, claudication, peripheral occlusive arterial disease, atherosclerosis, thrombotic or thromboembolic conditions, or CNS disorders associated with cerebral ischaemia. The present sequence represents the human MK2 variant 2, which is located on chromosome 1q32.  
XX  
SQ Sequence 400 AA;  
Query Match 99.6%; Score 2097; DB 8; Length 400;  
Best Local Similarity 99.7%; Pred. No. 1.1e-160;  
Matches 395; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 SQGSPVPVPPAPPPQPPPTPALPHPPAQQPPPPQPPQPPHVKSLQIKKNAIIDDYK 60  
Db 5 SQGSPVPVPPAPPPQPPPTPALPHPPAQQPPPPQPPQPPHVKSLQIKKNAIIDDYK 64  
Qy 61 VTSQVLGLGINGKVLQIFNKRTQEKFALKMLQDCPKARREVELHWRASQCPHIVRVDVY 120  
Db 65 VTSQVLGLGINGKVLQIFNKRTQEKFALKMLQDCPKARREVELHWRASQCPHIVRVDVY 124  
Qy 121 ENLYAGRKCLLIWMECLDGGELFSRIQDRGDQAFTEREASEIMKSGEAIQYLSINIAH 180  
Db 125 ENLYAGRKCLLIWMECLDGGELFSRIQDRGDQAFTEREASEIMKSGEAIQYLSINIAH 184  
Qy 181 RDVKPENLLYTSKRPNAILKLTDFGAKETTSNLSLTPCYTPYYVAPEVLGPEKYDKSC 240  
Db 185 RDVKPENLLYTSKRPNAILKLTDFGAKETTSNLSLTPCYTPYYVAPEVLGPEKYDKSC 244  
Qy 241 DMWSLGVIMVILLCGVPPFVSNHGLAISPGMKTRIRMGQYEFNPNPSEVSEVKMLRN 300  
Db 245 DMWSLGVIMVILLCGVPPFVSNHGLAISPGMKTRIRMGQYEFNPNPSEVSEVKMLRN 304  
Qy 301 LLKTEPTQRMITTEFMNHPIMOSTKVPQTPPLHTSRVLKEDKERWEDVKEEMTSALATMR 360  
Db 305 LLKTEPTQRMITTEFMNHPIMOSTKVPQTPPLHTSRVLKEDKERWEDVKEEMTSALATMR 364  
Qy 361 VDYEQIKIKKIEDASNPILLKRRKKARALEAALAH 396  
Db 365 VDYEQIKIKKIEDASNPILLKRRKKARALEAALAH 400

RESULT 8  
ADX06660  
ID ADX06660 standard; protein; 400 AA.  
XX  
XX ADX06660;  
XX  
XX 21-APR-2005 (first entry)  
XX  
XX Cyclin-dependent kinase modulation biomarker SEQ ID NO 1225.  
XX  
XX cytotstatic; cyclin-dependent kinase; cdk; biomarker.  
XX  
XX Homo sapiens.  
XX  
XX W02005012875-A2.  
XX  
XX 10-FEB-2005.  
XX  
XX 29-JUL-2004; 2004WO-US024424.  
XX  
XX 29-JUL-2003; 2003US-0490890P.  
XX  
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.  
XX  
XX Li M, Rupnow BA, Webster KR, Jackson DG, Wong TW;  
XX WPI; 2005-163068/17.  
XX  
XX N-PSDB; ADX06659.  
XX  
XX Biomarkers useful for predicting or determining the response of a mammal  
PT to a cancer treatment comprising administration of a modulator of cyclin-  
XX dependent kinase activity.  
XX

PS Claim 5; SEQ ID NO 1225; 141pp; English.

XX This invention describes a novel method of predicting or determining  
CC whether a mammal will respond or is responding to an anti-cancer agent  
CC that modulates cyclin-dependent kinase (cdk) activity. The method  
CC comprises measuring the level of one or more biomarkers selected from  
CC 2774 biomarkers given in the specification (nucleotide sequence SEQ ID  
CC NO:1246 (Genbank EST W28729) is especially preferred). The method of the  
CC invention is utilized in a kit for determining or predicting whether  
CC patient would be susceptible or resistant to treatment by an agent  
CC modulating cdk activity. The invention also describes a method for  
CC utilizing individualized genetic profiles for treating diseases and  
CC disorders based on patient's response and molecular level, specialized  
CC microarrays comprising the biomarkers described, antibodies directed  
CC against the biomarkers and a cell culture model to identify biomarkers.  
CC The cdk modulator is preferably N-5-[(5-(1,1-dimethylethyl)-2-  
CC oxazolyl)methylthio]-2-thiazolyl-4-piperidine carboxamide, 0.5-L-  
CC tartaric acid salt. Note: The sequence data for this patent did not form  
CC part of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences. This  
CC sequence represents a biomarker used in the method of the invention.

XX SQ Sequence 400 AA;

Query Match 99.6%; Score 2097; DB 9; Length 400;  
Best Local Similarity 99.7%; Pred. No. 1.1e-160;  
Matches 395; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SQGSPVPVPPAPAPPQPTPALPHPPAPQPPPPQPFQFHVKSGLIQKNAIIDYK 60  
DB 5 SQGSPVPVPPAPAPPQPTPALPHPPAPQPPPPQPFQFHVKSGLIQKNAIIDYK 64

QY 61 VTSQVLGLGKNGKVLQIFNKRQKFKALKMLQDCPKARREVELHWRASQCPHIVRVDVY 120  
DB 65 VTSQVLGLGKNGKVLQIFNKRQKFKALKMLQDCPKARREVELHWRASQCPHIVRVDVY 124

QY 121 ENLYAGRKCLLIWNECLDGGELFSRIQDRGQDQAFEREASEIMKSIGEAQYLSINIAH 180  
DB 125 ENLYAGRKCLLIWNECLDGGELFSRIQDRGQDQAFEREASEIMKSIGEAQYLSINIAH 184

QY 181 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSNLSLTPCPTYVYVAPEVLGPPEYDKSC 240  
DB 185 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSNLSLTPCPTYVYVAPEVLGPPEYDKSC 244

QY 241 DMWSLGVIMYILLCGYPPFYSNHGLAISPQMKTRIRMGQYEFPPNPSEVSEEVKMLIRN 300  
DB 245 DMWSLGVIMYILLCGYPPFYSNHGLAISPQMKTRIRMGQYEFPPNPSEVSEEVKMLIRN 304

QY 301 LLKTEPTQRTMITFEMNHPWIMQSTKVPQTPPLHTSRVLKEDKRWEDVKEMTSALATMR 360  
DB 305 LLKTEPTQRTMITFEMNHPWIMQSTKVPQTPPLHTSRVLKEDKRWEDVKEMTSALATMR 364

QY 361 VDYEQIKIKKIEDASNPILLKRRKKARALEAAALAH 396  
DB 365 VDYEQIKIKKIEDASNPILLKRRKKARALEAAALAH 400

RESULT 9  
ADE60496  
ID ADE60496 standard; protein; 385 AA.  
XX AC ADE60496;  
XX XX  
XX 29-JAN-2004 (first entry)  
XX DE Rat Protein CAA54183, SEQ ID NO 6405.  
XX KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
XX KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.  
XX OS Rattus norvegicus.  
XX XX  
XX PN WO2003016475-A2.

XX PD 27-FEB-2003.

XX PF 14-AUG-2002; 2002WO-US025765.

XX PR 14-AUG-2001; 2001US-0312147P.  
XX PR 01-NOV-2001; 2001US-0346382P.  
XX PR 26-NOV-2001; 2001US-0333347P.

XX PA (GEHO ) GEN HOSPITAL CORP.  
XX PA (FARB ) BAYER AG.

XX PI Woolf C, D'urso D, Befort K, Costigan M;  
XX DR WPI: 2003-268312/26.  
XX DR GENBANK; CAA54183.

XX New composition comprising two or more isolated polypeptides, useful for  
XX preparing a medicament for treating pain in an animal.

XX PS Claim 1; Page; 1017pp; English.

XX CC The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a rat protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 385 AA;

Query Match 91.2%; Score 1921; DB 7; Length 385;  
Best Local Similarity 92.7%; Pred. No. 1.7e-146;  
Matches 367; Conservative 7; Mismatches 8; Indels 14; Gaps 2;

QY 1 SQGSPVPVPPAPAPPQPTPALPHPPAPQPPPPQPFQFHVKSGLIQKNAIIDYK 60  
DB 4 SPQSTPPAPPSPSPPP-----APAPPPP-----FQFHVKSGLIQKNAIIDYK 49

QY 61 VTSQVLGLGKNGKVLQIFNKRQKFKALKMLQDCPKARREVELHWRASQCPHIVRVDVY 120  
DB 50 VTSQVLGLGKNGKVLQIFNKRQKFKALKMLQDCPKARREVELHWRASQCPHIVRVDVY 109

QY 121 ENLYAGRKCLLIWNECLDGGELFSRIQDRGQDQAFEREASEIMKSIGEAQYLSINIAH 180  
DB 110 ENLYAGRKCLLIWNECLDGGELFSRIQDRGQDQAFEREASEIMKSIGEAQYLSINIAH 169

QY 181 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSNLSLTPCPTYVYVAPEVLGPPEYDKSC 240  
DB 170 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSNLSLTPCPTYVYVAPEVLGPPEYDKSC 229

QY 241 DMWSLGVIMYILLCGYPPFYSNHGLAISPQMKTRIRMGQYEFPPNPSEVSEEVKMLIRN 300

||||| 230 DMWSLGVIMYLLCGYPFFYSNHGLAISPGMKTRIRMGQYEFNPEWSEVSEVKMLIRN 289  
||||| 301 LLKTEPTQRTMTITEFNMHPWIMOSTKVPQTPPLHTSRVLKEDKERWEDVKEEMTSALATMR 360  
||||| 290 LLKTEPTQRTMTITEFNMHPWIMOSTKVPQTPPLHTSRVLKEDKERWEDVKEEMTSALATMR 349  
361 VDYEQIKIKKIEDASNPPLLLKRRKKARALEAALAH 396  
350 VDYEQIKIKKIEDASNPPLLLKRRKKARAVEDAALAH 385

RESULT 10  
ADD47657  
ID ADD47657 standard; protein; 385 AA.  
XX  
AC ADD47657;  
DT 02-DEC-2004 (revised)  
DT 29-JAN-2004 (first entry)  
XX  
XX Rat Protein CAA54183, SEQ ID NO 13353.  
DE  
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.  
KW  
XX Rattus norvegicus.  
OS  
XX Unidentified.  
XX  
XX W02003016475-A2.  
XX  
XX 27-FEB-2003.  
XX  
XX 14-AUG-2002; 2002WO-US025765.  
XX  
XX 14-NOV-2001; 2001US-0312147P.  
PR  
XX 01-NOV-2001; 2001US-0346382P.  
PR  
XX 26-NOV-2001; 2001US-0333347P.  
XX  
XX (GEHO ) GEN HOSPITAL CORP.  
PA  
XX (FARB ) BAYER AG.  
XX  
XX Woolf C, D'urso D, Befort K, Costigan M;  
XX  
XX WPT; 2003-268312/26.  
DR  
XX GENBANK; CAA54183.  
XX  
XX New composition comprising two or more isolated polypeptides, useful for  
PT preparing a medicament for treating pain in an animal.  
XX  
XX Example 1; Page; 1017pp; English.  
XX  
XX The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction

CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a rat protein (described in Table 3  
CC of the specification) which is differentially expressed during pain.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 385 AA;  
Query Match 91.2%; Score 1921; DB 7; Length 385;  
Best Local Similarity 92.7%; Pred. NO. 1.7e-146;  
Matches 367; Conservative 7; Mismatches 8; Indels 14; Gaps 2;  
QY 1 SQQSPPVPFPAPAPPPQPTPALPPPAQPPPPPPQPPQPFHVKSLQIKKNAITDDYK 60  
DB 4 SPQQTTPAPPPSPPPP-----APAQPPPP-----FPQFHVKSLQIRKNAITDDYK 49  
QY 61 VTSQVLGLGINGKVLQIFNKRTQEKFALKMLQDCPKARREVELHWRASQCPHIVRIVDVY 120  
DB 50 VTSQVLGLGINGKVLRFIDKRTQOKFALKMLQDCPKARREVELTWASQCPHIVRIVDVY 109  
QY 121 ENLYAGRKCLLIWMECLDGELFSRIODRGDQAFTEREASEIMKSGEAIQYLHSINIAH 180  
DB 110 ENLYAGRKCLLIWMECLDGELFSRIODRGDQAFTEREASEIMKSGEAIQYLHSINIAH 169  
QY 181 RDVKPENLLYTSKRPNAILKLTDFGAKETTSNSLTTPCYTPYYVAPEVLGPEKDYKSC 240  
DB 170 RDVKPENLLYTSKRPNAILKLTDFGAKETTSNSLTTPCYTPYYVAPEVLGPEKDYKSC 229  
QY 241 DMWSLGVIMYLLCGYPFFYSNHGLAISPGMKTRIRMGQYEFNPEWSEVSEVKMLIRN 300  
DB 230 DMWSLGVIMYLLCGYPFFYSNHGLAISPGMKTRIRMGQYEFNPEWSEVSEVKMLIRN 289  
QY 301 LLKTEPTQRTMTITEFNMHPWIMOSTKVPQTPPLHTSRVLKEDKERWEDVKEEMTSALATMR 360  
DB 290 LLKTEPTQRTMTITEFNMHPWIMOSTKVPQTPPLHTSRVLKEDKERWEDVKEEMTSALATMR 349  
QY 361 VDYEQIKIKKIEDASNPPLLLKRRKKARALEAALAH 396  
DB 350 VDYEQIKIKKIEDASNPPLLLKRRKKARAVEDAALAH 385

RESULT 11  
ABM82670  
ID ABM82670 standard; protein; 378 AA.  
XX  
AC ABM82670;  
XX  
DT 18-NOV-2004 (first entry)  
XX  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:2919.  
XX  
XX gene therapy; human diagnostic and therapeutic polynucleotide; dthcp.  
XX Homo sapiens.  
XX  
XX W02004023973-A2.  
XX  
XX 25-MAR-2004.  
XX  
XX 12-SEP-2003; 2003WO-US028227.  
XX  
XX 12-SEP-2002; 2002US-0410259P.  
PR  
XX 12-SEP-2002; 2002US-0410260P.  
XX  
XX (INCY-) INCYTE CORP.  
XX  
XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;  
PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;  
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;  
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;  
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;  
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirtson ES;

PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;  
 PI Patury S, Shi X, Suarez CJ;  
 XX WPI: 2004-329368/30.  
 DR N-PSDB; ACN41322.  
 XX New diagnostic and therapeutic polynucleotides and polypeptides, useful  
 PT in diagnosing a condition, disease or disorder associated with human  
 PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or  
 PT in gene mapping.  
 XX Claim 27; Page: 190pp; English.  
 PS  
 XX The invention relates to novel diagnostic and therapeutic polynucleotides  
 CC selected from one of the 2722 sequences defined in the specification. A  
 CC polynucleotide of the invention may have a use in gene therapy. The human  
 CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be  
 CC used to diagnose a particular condition, disease or disorder associated  
 CC with human molecules, e.g. cell proliferative disorders,  
 CC autoimmune/inflammatory disorder, developmental disorder, endocrine  
 CC disorder, neurological disorders, gastrointestinal disorders, or  
 CC infections caused by virus, bacteria, fungi or parasite. The dithp  
 CC molecules may also be used in genetic mapping, in identifying individuals  
 CC from minute biological samples, in detecting single nucleotide  
 CC polymorphisms, as molecular weight markers, and for somatic or germline  
 CC gene therapy. The present sequence represents a dithp protein of the  
 CC invention. Note: The sequence data for this patent is not represented in  
 CC the printed specification, but was obtained in electronic format directly  
 CC from WIPO at [www.wipo.int/pct/en/sequences/listing.htm](http://www.wipo.int/pct/en/sequences/listing.htm)  
 XX  
 SQ Sequence 378 AA;

Query Match 89.6%; Score 1886; DB 8; Length 378;  
 Best Local Similarity 99.2%; Pred. No. 1.1e-143;  
 Matches 350; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SQSQSPVPFPAPAPPQPTPALPHPPAQPQPPPPQFPQFHVKSGLQIKKNAIIDDYK 60  
 DB 5 SQSQSPVPFPAPAPPQPTPALPHPPAQPQPPPPQFPQFHVKSGLQIKKNAIIDDYK 64  
 QY 61 VTSQVLGLGNGKVLQIFNKRTOEKFPALQMDQCPKARREVELHWRASQCPHIVRVDVY 120  
 DB 65 VTSQVLGLGNGKVLQIFNKRTOEKFPALQMDQCPKARREVELHWRASQCPHIVRVDVY 124  
 QY 121 ENLYAGRKCLLIWECLDGGELFSRIQDRGDOAFTEREASEIMKSGEALQYLSHNIAH 180  
 DB 125 ENLYAGRKCLLIWECLDGGELFSRIQDRGDOAFTEREASEIMKSGEALQYLSHNIAH 184  
 QY 181 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSNLSLTPCYTPYYVAPEVLGPEKDKSC 240  
 DB 185 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSNLSLTPCYTPYYVAPEVLGPEKDKSC 244  
 QY 241 DMWSLGVIMYLLCGYPPFYSNHLAISPGMKTRIRMGQYEFNPNPSEVSEVSKMLRN 300  
 DB 245 DMWSLGVIMYLLCGYPPFYSNHLAISPGMKTRIRMGQYEFNPNPSEVSEVSKMLRN 304  
 QY 301 LLKTEPTQRMWITTEFMNHPWIMQSTKVPOTPLHTSRVLKEDKERWEDVKEMT 353  
 DB 305 LLKTEPTQRMWITTEFMNHPWIMQSTKVPOTPLHTSRVLKEDKERWEDVKEMT 357

RESULT 12

ABP54949  
 ID ABP54949 standard; protein; 370 AA.  
 XX  
 AC ABP54949;  
 XX  
 DT 13-JAN-2003 (first entry)  
 XX  
 DE Human MAPKAP kinase 2.  
 XX  
 KW MAPKAP kinase 2; tyrosine threonine kinase; TTK; protein kinase; enzyme;  
 KW mitotic checkpoint; colon cancer; breast cancer; tumour; cytostatic;

KW human; gene therapy.  
 XX Homo sapiens.  
 XX WO200268444-A1.  
 XX 06-SEP-2002.  
 XX 21-FEB-2002; 2002WO-US005278.  
 XX 21-FEB-2001; 2001US-0271254P.  
 XX (CHIR ) CHIRON CORP.  
 XX Reinhard C, Jefferson AB, Chan VW;  
 XX WPI: 2002-698650/75.  
 DR N-PSDB; ABV73995.  
 XX Reducing growth of cancer cells comprises reducing Tyrosine Threonine  
 PT Kinase (TTK) activity, useful in diagnosing and treating disorders with  
 PT abnormal expression levels and activity of TTK, such as lung, colon,  
 PT prostate and ovarian cancer.

PS Disclosure; Page 108; 113pp; English.

XX The present sequence is the protein sequence of human MAPKAP kinase 2.  
 CC This is an example of a gene product that is differentially expressed in  
 CC cancer cells relative to non-cancer cells, or between cancer cells of  
 CC different malignant potential. Such genes, and their gene products, can  
 CC be assayed in addition to tyrosine threonine kinase (TTK, see ABP54938),  
 CC in methods of the invention for differential expression in a test cell.  
 CC The invention is based on the finding that TTK is differentially  
 CC expressed in various forms of cancer. Methods are provided for the  
 CC identification of cancerous cells, especially breast cancer and colon  
 CC cancer cells, by detection of expression levels of TTK, as well as  
 CC diagnostic, prognostic and therapeutic methods based on differential  
 CC expression. These methods can be used as the basis of rational therapy.  
 CC Assays for identifying molecules that modulate the activity of these  
 CC genes in cancers, as well as methods of inhibiting tumour growth by  
 CC inhibiting the activity of TTK are also provided

XX Sequence 370 AA;

Query Match 89.4%; Score 1882; DB 5; Length 370;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-143;  
 Matches 349; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQSQSPVPFPAPAPPQPTPALPHPPAQPQPPPPQFPQFHVKSGLQIKKNAIIDDYK 60  
 DB 5 SQSQSPVPFPAPAPPQPTPALPHPPAQPQPPPPQFPQFHVKSGLQIKKNAIIDDYK 64  
 QY 61 VTSQVLGLGNGKVLQIFNKRTOEKFPALQMDQCPKARREVELHWRASQCPHIVRVDVY 120  
 DB 65 VTSQVLGLGNGKVLQIFNKRTOEKFPALQMDQCPKARREVELHWRASQCPHIVRVDVY 124  
 QY 121 ENLYAGRKCLLIWECLDGGELFSRIQDRGDOAFTEREASEIMKSGEALQYLSHNIAH 180  
 DB 125 ENLYAGRKCLLIWECLDGGELFSRIQDRGDOAFTEREASEIMKSGEALQYLSHNIAH 184  
 QY 181 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSNLSLTPCYTPYYVAPEVLGPEKDKSC 240  
 DB 185 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSNLSLTPCYTPYYVAPEVLGPEKDKSC 244  
 QY 241 DMWSLGVIMYLLCGYPPFYSNHLAISPGMKTRIRMGQYEFNPNPSEVSEVSKMLRN 300  
 DB 245 DMWSLGVIMYLLCGYPPFYSNHLAISPGMKTRIRMGQYEFNPNPSEVSEVSKMLRN 304  
 QY 301 LLKTEPTQRMWITTEFMNHPWIMQSTKVPOTPLHTSRVLKEDKERWEDVKEMT 349  
 DB 305 LLKTEPTQRMWITTEFMNHPWIMQSTKVPOTPLHTSRVLKEDKERWEDVKEMT 353

## RESULT 13

ABU61622  
ID ABU61622 standard; protein; 370 AA.

XX AC ABU61622;  
XX DT 11-AUG-2003 (first entry)  
XX Human cancer-expressed protein MAPKAP kinase 2.  
XX DE Human; enzyme; tyrosine threonine kinase; TTK; cancer; cytotostatic;  
XX KW mitotic checkpoint gene; MAPKAP kinase 2.  
XX OS Homo sapiens.  
XX PN US2003045491-A1.

XX PD 06-MAR-2003.

XX PF 21-FEB-2002; 2002US-00081119.

XX PR 23-FEB-2001; 2001US-0289813P.

XX PA (REIN/) REINHARD C.

XX PA (JEFF/) JEFFERSON A B.

XX PA (CHAN/) CHAN V W.

XX PI Reinhard C, Jefferson AB, Chan VW;

XX DR WPI; 2003-456566/43.

XX DR N-PSDB; ACA62272.

XX Detecting cancer in a subject, by comparing expression levels of tyrosine  
PT threonine kinase polypeptide or polynucleotide in a subject cell and a  
PT normal cell, where an increase in the expression level in the test cell  
PT is indicative of cancer.

XX PS Disclosure; Page 61-62; 79pp; English.

XX The invention relates to detecting cancer (other than ovarian cancer) in  
CC a subject, comprising comparing the expression levels of tyrosine  
CC threonine kinase (TTK, a mitotic checkpoint gene) polypeptide or  
CC polynucleotide in a test cell obtained from the subject and in a normal  
CC non-cancer cell, where an increase in the expression level of TTK protein  
CC or nucleic acid in the test cell compared to that in the normal cell,  
CC indicates the presence of cancer other than ovarian cancer. Also included  
CC are reducing growth of a cancerous cell (by contacting a cancerous cell  
CC with an amount of an agent effective to reduce TTK polypeptide activity  
CC in the cell), an assay for identifying a candidate agent that reduces  
CC growth of a cancerous cell (comprising: (i) detecting the activity of a  
CC TTK polypeptide in the presence of a candidate agent; and (ii) comparing  
CC the activity of TTK polypeptide in the presence of a candidate agent  
CC relative to TTK polypeptide activity in the absence of the candidate  
CC agent), identifying an agent that reduces TTK activity (comprising: (i)  
CC contacting a cancerous cell displaying elevated expression of a TTK-  
CC encoding polynucleotide with a candidate agent; and (ii) determining the  
CC effect of the candidate agent on TTK polypeptide activity) and assessing  
CC the prognosis of a cancerous disease other than ovarian cancer in a  
CC subject (comprising: (i) detecting expression of TTK -encoding  
CC polynucleotide in a test cancer cell of a subject; and (ii) comparing a  
CC level of expression of TTK-encoding polynucleotide in the test cancer  
CC cell with a level of expression of the polynucleotide in a control non-  
CC cancer cell, where the level of expression of TTK in the test cancer cell  
CC relative to the level of expression in the control non-cancer cell is  
CC indicative of the prognosis of the cancerous disease). The methods are  
CC useful for detecting cancer (other than ovarian cancer) in a subject,  
CC reducing growth of cancerous cells, identifying a candidate agent that  
CC reduces growth of a cancerous cell, identifying an agent that reduces TTK  
CC activity and assessing the prognosis of a cancerous disease other than  
CC ovarian cancer. The methods are also useful for determining the ability  
CC of a subject to respond to a particular therapy e.g. as a basis of  
CC rational therapy. The present sequence represents another protein which  
CC is differentially expressed in cancer tissues, in this case human MAPKAP

CC kinase 2  
XX XX  
SQ Sequence 370 AA;  
  
Query Match 89.4%; Score 1882; DB 7; Length 370;  
Best Local Similarity 100.0%; Pred. No. 2,3e-143;  
Matches 349; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SQSQSPVPFPAPAPPQPTPALPHPPAQPAPPPPPQFPQFHVKSGLOIKKNAIIDDYK 60  
DB 5 SQSQSPVPFPAPAPPQPTPALPHPPAQPAPPPPPQFPQFHVKSGLOIKKNAIIDDYK 64  
QY 61 VTSQVLGLGINGKVLQIFNKRTQEKALKMLQDCPKARREVELHWRASQCPHIVRVDVY 120  
DB 65 VTSQVLGLGINGKVLQIFNKRTQEKALKMLQDCPKARREVELHWRASQCPHIVRVDVY 124  
QY 121 ENLYAGRKCLLIWMECLDGGELFSRIQDRGDOAFTEREASEIMKSGEAIQYLHSHINIAH 180  
DB 125 ENLYAGRKCLLIWMECLDGGELFSRIQDRGDOAFTEREASEIMKSGEAIQYLHSHINIAH 184  
QY 181 RDVKPENLLYTSKRPNAILKLTDFGPAKETTSNSLTTPCYTPYYVAPEVLGPEKYDKSC 240  
DB 185 RDVKPENLLYTSKRPNAILKLTDFGPAKETTSNSLTTPCYTPYYVAPEVLGPEKYDKSC 244  
QY 241 DMWSLGVIMYILLCGYPPEYSNHGLAISPGMKTRIRMGQYEPENPSEVSEVKMLIRN 300  
DB 245 DMWSLGVIMYILLCGYPPEYSNHGLAISPGMKTRIRMGQYEPENPSEVSEVKMLIRN 304  
QY 301 LKTEPTQRMWTFTEFNNHPWIMQSTKVPQTPPLHTSRVLKEDKERWEDVK 349  
DB 305 LKTEPTQRMWTFTEFNNHPWIMQSTKVPQTPPLHTSRVLKEDKERWEDVK 353  
  
RESULT 14  
ADM36338  
ID ADM36338 standard; protein; 370 AA.  
XX AC ADM36338;  
XX DT 03-JUN-2004 (first entry)  
XX Human MK2 variant 1 protein SEQ ID NO:2.  
XX ischaemic injury;  
KW Mitogen-activated protein kinase-activated protein kinase 2; MK2;  
KW vasotropic; cerebroprotective; cardiac; hypotensive;  
KW antiarteriosclerotic; thrombolytic; neuroprotective; cardiovascular;  
KW antianginal; antiarrhythmic; MK2 antagonist; cerebral ischaemia;  
KW ischaemia; vascular occlusion; cerebral infarction; stroke;  
KW cerebral vascular disease; myocardial infarction;  
KW coronary artery disease; congestive heart failure; cardiac arrhythmia;  
KW unstable angina; high blood pressure; claudication;  
KW peripheral occlusive arterial disease; atherosclerosis;  
KW thrombotic condition; thromboembolic condition; CNS disorder; human;  
KW MK2 variant 1; chromosome 1q32.  
XX OS Homo sapiens.  
XX PN WO2004017909-A2.  
XX PD 04-MAR-2004.  
XX PF 21-AUG-2003; 2003WO-US026337.  
XX PR 23-AUG-2002; 2002US-0405586P.  
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.  
XX PI Wang X, Schieven G, Feuerstein GZ;  
XX WPI; 2004-226726/21.  
XX DR N-PSDB; ADM36337.



PT Reducing or treating ischemic injury, comprises administering an  
PT inhibitor of mitogen-activated protein kinase-activated protein kinase 2  
PT (MK2) activity or expression.  
XX  
XX Disclosure; SEQ ID NO 2; 39pp; English.  
XX  
XX The present invention describes a method for reducing ischaemic injury in  
CC a mammal, which comprises administering a compound that reduces the  
CC activity of mitogen-activated protein kinase-activated protein kinase 2  
CC (MK2) or that inhibits MK2 expression. Also described: (1) identifying a  
CC compound which inhibits MK2 expression in a cell, or which modulates MK2  
CC activity; (2) compounds identified by the method above; and (3) treating  
CC ischaemic injury by administering to a patient a compound above, or an  
CC MK2 modulator. The compound has vasotropic, cerebroprotective, cardiac,  
CC hypotensive, antiarteriosclerotic, thrombolytic, neuroprotective,  
CC cardiovascular, antianginal and antiarrhythmic activities, and can be  
CC used as an MK2 antagonist. The method is useful reducing or treating  
CC ischaemic injury, particularly cerebral ischaemia. Compounds identified  
CC by the method are useful for treating ischaemia, (e.g. ischaemia  
CC resulting from vascular occlusion, cerebral infarction, stroke, and  
CC related cerebral vascular diseases), myocardial infarction, coronary  
CC artery disease, congestive heart failure, cardiac arrhythmias, unstable  
CC angina, high blood pressure, claudication, peripheral occlusive arterial  
CC disease, atherosclerosis, thrombotic or thromboembolic conditions, or CNS  
CC disorders associated with cerebral ischaemia. The present sequence  
CC represents the human MK2 variant 1, which is located on chromosome 1q32.  
XX  
XX  
SQ Sequence 370 AA;

Query Match 89.4%; Score 1882; DB 8; Length 370;  
Best Local Similarity 100.0%; Pred. No. 2.3e-143;  
Matches 349; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 SQGSPVPFPAPAPPQPTPALPHPPAQPDPPPPPQPFQFHVKSLQIKKNAIIDYK 60  
Db 5 SQGSPVPFPAPAPPQPTPALPHPPAQPDPPPPPQPFQFHVKSLQIKKNAIIDYK 64  
Qy 61 VTSQVLGLGNGKVLQIFNKRTOEKFKALQMDQCPKARREVELHWRASQCPHIVRVDVY 120  
Db 65 VTSQVLGLGNGKVLQIFNKRTOEKFKALQMDQCPKARREVELHWRASQCPHIVRVDVY 124  
Qy 121 ENLYAGRKCLLIYMECLDGGELFSRIQDRGQDAFTEREASEIMKSIGEAIOYLSINIAH 180  
Db 125 ENLYAGRKCLLIYMECLDGGELFSRIQDRGQDAFTEREASEIMKSIGEAIOYLSINIAH 184  
Qy 181 RDVKNPENVLTSKPNAILKLTDFGFAKETSHNSLTTPCYTYYVAPEVLGPPEYDKSC 240  
Db 185 RDVKNPENVLTSKPNAILKLTDFGFAKETSHNSLTTPCYTYYVAPEVLGPPEYDKSC 244  
Qy 241 DMWSLGVIMYILLGYPFPYSNHLGLAISPGMKTRIRMGQYFPPNPENVESEEVKMLIRN 300  
Db 245 DMWSLGVIMYILLGYPFPYSNHLGLAISPGMKTRIRMGQYFPPNPENVESEEVKMLIRN 304  
Qy 301 LLKTEPTQRMITTEFMNHPIMQSTKVPQTPPLHSTRVLKEDKERWEDVK 349  
Db 305 LLKTEPTQRMITTEFMNHPIMQSTKVPQTPPLHSTRVLKEDKERWEDVK 353

## RESULT 15

ADP87579  
ID ADP87579 standard; protein; 370 AA.

XX AC ADP87579;  
XX  
XX 23-SEP-2004 (first entry)  
XX DE Human NOVX polypeptide, NOV3a.  
XX  
XX anorectic; antidiabetic; gene therapy; vaccine; obesity; diabetes;  
KW insulin resistance; hybridization probe; chromosome mapping;  
KW tissue typing; preventive medicine; pharmacogenomics; NOVX; human.  
XX  
OS Homo sapiens.

Query Match 89.4%; Score 1882; DB 8; Length 370;  
Best Local Similarity 100.0%; Pred. No. 2.3e-143;  
Matches 349; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 SQGSPVPFPAPAPPQPTPALPHPPAQPDPPPPPQPFQFHVKSLQIKKNAIIDYK 60  
Db 5 SQGSPVPFPAPAPPQPTPALPHPPAQPDPPPPPQPFQFHVKSLQIKKNAIIDYK 64  
Qy 61 VTSQVLGLGNGKVLQIFNKRTOEKFKALQMDQCPKARREVELHWRASQCPHIVRVDVY 120  
Db 65 VTSQVLGLGNGKVLQIFNKRTOEKFKALQMDQCPKARREVELHWRASQCPHIVRVDVY 124  
Qy 121 ENLYAGRKCLLIYMECLDGGELFSRIQDRGQDAFTEREASEIMKSIGEAIOYLSINIAH 180

XX WO2004056961-A2.  
XX  
XX 08-JUL-2004.  
XX  
XX 27-OCT-2003; 2003WO-US034114.  
XX  
XX 25-OCT-2002; 2002US-0421239P.  
XX 28-OCT-2002; 2002US-0421700P.  
XX 31-OCT-2002; 2002US-0422776P.  
XX 13-NOV-2002; 2002US-0426197P.  
XX 20-DEC-2002; 2002US-0435498P.  
XX 20-DEC-2002; 2002US-0435510P.  
XX 21-DEC-2002; 2002US-0435568P.  
XX 21-MAR-2003; 2003US-0456812P.  
XX (CURA-) CURAGEN CORP.  
XX  
XX Berghs C, Catterton E, Ellerman K, Ort T, Rieger D, Chaudhuri A;  
XX WPI: 2004-500293/47.  
XX N-PSDB; ADP87579.  
XX  
XX New NOVX nucleic acid molecules and polypeptides useful for preventing or  
PT treating NOVX-associated disorders, e.g. diabetes, insulin resistance or  
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.  
XX  
XX Claim 3; SEQ ID NO 34; 570pp; English.

XX The invention relates to a novel isolated nucleic acid molecule  
CC comprising any of the nucleotide sequences (e.g. 3634, 2127 or 2120 base  
CC pairs) fully defined in the specification; or encodes any of the amino  
CC acid sequences (e.g. 698, 702 or 709 amino acids) fully defined in the  
CC specification. The invention further comprises: an isolated polypeptide  
CC comprising any of the amino acid sequences cited above; a method for  
CC identifying compounds that modulate target polypeptide activity; an  
CC antibody that immunospecifically binds to the target polypeptide; where  
CC the target polypeptide comprises any of the above-mentioned amino acid  
CC sequences, an amino acid sequence that is at least 95% identical to the  
CC above amino acid sequences, an amino acid sequence of at least one domain  
CC of the above-mentioned amino acid sequences, or an amino acid sequence  
CC that is at least 95% identical to the domain of the above amino acid  
CC sequences; a method for identifying a potential therapeutic agent for use  
CC in treatment of a pathology, where the pathology is related to aberrant  
CC expression or aberrant physiological interactions of a target polypeptide  
CC; and a method of screening for a modulator of activity of or of latency  
CC or predisposition to a pathology associated with a target polypeptide.  
CC The modulating compounds have anorectic and antidiabetic activities. The  
CC nucleic acid sequences of the invention may be used in gene therapy to  
CC treat disorders. The proteins of the invention may be used in creating a  
CC vaccine. The composition and methods of the invention may be used in creating a  
CC that modulate protein activity or for diagnosing, preventing or treating  
CC diverse pathological conditions, such as obesity, diabetes or insulin  
CC resistance. The nucleic acids are also used as hybridization probes, in  
CC chromosome mapping, tissue typing, preventive medicine, and  
CC pharmacogenomics. This sequence represents a NOVX polypeptide of the  
CC invention.

Sequence 370 AA;



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OM protein - protein search, using sw model

Run on: June 19, 2006, 09:12:12 ; Search time 188 Seconds  
(without alignments)  
975.708 Million cell updates/sec

Title: US-10-469-221-2

Perfect score: 2106

Sequence: 1 SQGQSPVPFPAPAPPPQPP.....PLLLKRRKARALEAAALAH 396

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA\_Main:\*

- 1: /EMC\_Celestra\_SID33/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /EMC\_Celestra\_SID33/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 3: /EMC\_Celestra\_SID33/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*
- 4: /EMC\_Celestra\_SID33/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 5: /EMC\_Celestra\_SID33/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 6: /EMC\_Celestra\_SID33/ptodata/2/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2106	100.0	396	4	US-10-469-221-2
2	2106	100.0	400	4	US-10-116-649-1
3	2106	100.0	400	4	US-10-294-027-1
4	2106	100.0	400	4	US-10-469-221-4
5	2106	100.0	400	5	US-10-497-767-1
6	2097	99.6	400	4	US-10-645-190-4
7	1882	89.4	370	4	US-10-081-119-34
8	1882	89.4	370	4	US-10-645-190-2
9	1882	89.4	370	5	US-10-951-389-34
10	1882	89.4	370	5	US-10-951-406-34
11	1882	89.4	370	5	US-10-977-077-34
12	1882	89.4	370	5	US-10-977-087-34
13	1833	87.0	357	4	US-10-664-421-114
14	1833	87.0	357	5	US-10-941-635-115
15	1729	82.1	327	4	US-10-116-649-2
16	1729	82.1	434	4	US-10-338-411-29
17	1729	82.1	434	4	US-10-389-640-29
18	1716	81.5	326	4	US-10-294-027-4
19	1391	66.0	382	4	US-10-294-027-2
20	1391	66.0	382	5	US-10-497-767-2
21	1391	66.0	382	5	US-10-501-035-352
22	1201	57.0	359	6	US-11-097-143-5664
23	1201	57.0	359	6	US-11-097-143-29037
24	1046	49.7	443	4	US-10-369-493-5950
25	995	47.2	197	3	US-09-925-300-1178
26	796.5	37.8	521	4	US-10-369-493-5500
27	733	34.8	471	5	US-10-770-726-68

28	733	34.8	471	6	US-11-152-366-31	Sequence 31, Appli
29	733	34.8	473	4	US-10-294-027-3	Sequence 3, Appli
30	733	34.8	473	6	US-11-152-366-32	Sequence 32, Appli
31	732	34.8	471	5	US-10-872-645-1	Sequence 1, Appli
32	540	25.6	484	4	US-10-408-765A-1218	Sequence 1218, Ap
33	536.5	25.5	612	4	US-10-437-963-139689	Sequence 139689,
34	534.5	25.4	339	4	US-10-664-421-113	Sequence 113, App
35	534.5	25.4	339	5	US-10-941-635-114	Sequence 114, App
36	514.5	24.4	332	4	US-10-664-421-13	Sequence 13, Appli
37	514.5	24.4	332	5	US-10-941-635-13	Sequence 3, Appli
38	514.5	24.4	332	5	US-10-497-767-3	Sequence 36, Appli
39	512.5	24.3	317	3	US-09-935-464-36	Sequence 36, Appli
40	512.5	24.3	317	4	US-10-125-835-36	Sequence 55, Appli
41	512.5	24.3	326	4	US-10-664-421-55	Sequence 55, Appli
42	512.5	24.3	326	5	US-10-941-635-55	Sequence 55, Appli
43	512.5	24.3	370	3	US-09-817-181-4	Sequence 4, Appli
44	512.5	24.3	370	3	US-09-769-970-19	Sequence 19, Appli
45	512.5	24.3	370	4	US-10-142-356-7	Sequence 7, Appli

#### ALIGNMENTS

#### RESULT 1

US-10-469-221-2

; Sequence 2, Application US/10469221

; Publication No. US20040170995A1

; GENERAL INFORMATION:

; APPLICANT: LOGRASSO, PHILIP

; APPLICANT: HAWKINS, JULIO

; APPLICANT: LISNOCK, JEAN MARIE

; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING

; TITLE OF INVENTION: A NOVEL HUMAN SIGNAL TRANSDUCING KINASE-MARKAP-2; ENCODED

; TITLE OF INVENTION: PROTEINS, CELLS TRANSFORMED THEREWITH AND USES THEREOF

; FILE REFERENCE: 20813P

; CURRENT APPLICATION NUMBER: US/10/469,221

; CURRENT FILING DATE: 2003-08-27

; PRIOR APPLICATION NUMBER: PCT/US02/05670

; PRIOR FILING DATE: 2002-02-25

; PRIOR APPLICATION NUMBER: 60/272,260

; PRIOR FILING DATE: 2001-02-28

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 396

; TYPE: PRT

; ORGANISM: Human

; US-10-469-221-2

Query Match 100.0%; Score 2106; DB 4; Length 396;

Best Local Similarity 100.0%; Pred. No. 4.5e-133;

Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQGQSPVPFPAPAPPPQPPPTPALPHPPAQQPPPPPPQPPPHVKSGLQIKKNAIIDDK 60

Db 1 SQGQSPVPFPAPAPPPQPPPTPALPHPPAQQPPPPPPQPPPHVKSGLQIKKNAIIDDK 60

QY 61 VTSQVLGLGKNGKVLQIENKRTQEKFKMLQDCPKARREVELHWRASCPHIVRVDVY 120

Db 61 VTSQVLGLGKNGKVLQIENKRTQEKFKMLQDCPKARREVELHWRASCPHIVRVDVY 120

QY 121 ENLYAGRKCLLIIVMECLDGGELFSRIQDRGQDAFTEREASEIMKSGIAGEIAIYLSHINIAH 180

Db 121 ENLYAGRKCLLIIVMECLDGGELFSRIQDRGQDAFTEREASEIMKSGIAGEIAIYLSHINIAH 180

QY 181 RDVKPENLYTSKRPNAILKLTDFGFAKETTSNLSLTTCYTPYVVAPEVLGPEKYDKSC 240

Db 181 RDVKPENLYTSKRPNAILKLTDFGFAKETTSNLSLTTCYTPYVVAPEVLGPEKYDKSC 240

QY 241 DMWSLGVIMYLLCGYPPFPFYSNHLGLAISPQMKTRIRMGQYEPNPENWSEVSEVKMLRN 300

Db 241 DMWSLGVIMYLLCGYPPFPFYSNHLGLAISPQMKTRIRMGQYEPNPENWSEVSEVKMLRN 300



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; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Human
US-10-469-221-4

Query Match          100.0%; Score 2106; DB 4; Length 400;
Best Local Similarity 100.0%; Pred. No. 4.5e-133;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQGSPVPVPPAPAPPQPPTPALPHPPAQPPTPPQPFQFHVKSGLIQKNAIIDDYK 60
Db 5 SQGSPVPVPPAPAPPQPPTPALPHPPAQPPTPPQPFQFHVKSGLIQKNAIIDDYK 64

Qy 61 VTSQVLGLGINGKVLQIFNKRTOEKFKALMLQDCPKARREVELHWRASQCPHIVRVDVY 120
Db 65 VTSQVLGLGINGKVLQIFNKRTOEKFKALMLQDCPKARREVELHWRASQCPHIVRVDVY 124

Qy 121 ENLYAGRKCLLIWMECLDGGELFSRIQDRGQAFTEREASEIMKSGEAIQYLHSINIAH 180
Db 125 ENLYAGRKCLLIWMECLDGGELFSRIQDRGQAFTEREASEIMKSGEAIQYLHSINIAH 184

Qy 181 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSNLSLTPCYTPYYVAPEVLGPEKYDKSC 240
Db 185 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSNLSLTPCYTPYYVAPEVLGPEKYDKSC 244

Qy 241 DMWSLGVIMYILLCGYPPFFYSNHGLAISPGMKTRIRMGQYEFPPNPSEVSEEVKMLRN 300
Db 245 DMWSLGVIMYILLCGYPPFFYSNHGLAISPGMKTRIRMGQYEFPPNPSEVSEEVKMLRN 304

Qy 301 LLKTEPTQRMITTEFNMHPWIMOSTKVPQTPPLHTSRVLKEDKERWEDVKEEMTSALATMR 360
Db 305 LLKTEPTQRMITTEFNMHPWIMOSTKVPQTPPLHTSRVLKEDKERWEDVKEEMTSALATMR 364

Qy 361 VDYEQIKIKKIEDASNPILLKRRKKARALEAAALAH 396
Db 365 VDYEQIKIKKIEDASNPILLKRRKKARALEAAALAH 400

RESULT 6
US-10-645-190-4
; Sequence 4, Application US/10645190
; Publication No. US20040110710A1
; GENERAL INFORMATION:
; APPLICANT: BRISTOL-MYERS SQUIBB COMPANY
; TITLE OF INVENTION: METHODS FOR PREVENTING ISCHEMIC BRAIN INJURY
; FILE REFERENCE: D0299 NP
; CURRENT APPLICATION NUMBER: US/10/645,190
; PRIOR FILING DATE: 2003-08-21
; PRIOR FILING DATE: 2002-08-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Human
US-10-645-190-4

Query Match          99.6%; Score 2097; DB 4; Length 400;
Best Local Similarity 99.7%; Pred. No. 1.8e-132;
Matches 395; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SQGSPVPVPPAPAPPQPPTPALPHPPAQPPTPPQPFQFHVKSGLIQKNAIIDDYK 60
Db 5 SQGSPVPVPPAPAPPQPPTPALPHPPAQPPTPPQPFQFHVKSGLIQKNAIIDDYK 64

Qy 61 VTSQVLGLGINGKVLQIFNKRTOEKFKALMLQDCPKARREVELHWRASQCPHIVRVDVY 120
Db 65 VTSQVLGLGINGKVLQIFNKRTOEKFKALMLQDCPKARREVELHWRASQCPHIVRVDVY 124

Qy 121 ENLYAGRKCLLIWMECLDGGELFSRIQDRGQAFTEREASEIMKSGEAIQYLHSINIAH 180
Db 125 ENLYAGRKCLLIWMECLDGGELFSRIQDRGQAFTEREASEIMKSGEAIQYLHSINIAH 184

Qy 181 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSNLSLTPCYTPYYVAPEVLGPEKYDKSC 240
Db 185 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSNLSLTPCYTPYYVAPEVLGPEKYDKSC 244

Qy 241 DMWSLGVIMYILLCGYPPFFYSNHGLAISPGMKTRIRMGQYEFPPNPSEVSEEVKMLRN 300
Db 245 DMWSLGVIMYILLCGYPPFFYSNHGLAISPGMKTRIRMGQYEFPPNPSEVSEEVKMLRN 304

Qy 301 LLKTEPTQRMITTEFNMHPWIMOSTKVPQTPPLHTSRVLKEDKERWEDVKEEMTSALATMR 360
Db 305 LLKTEPTQRMITTEFNMHPWIMOSTKVPQTPPLHTSRVLKEDKERWEDVKEEMTSALATMR 364

us-10-497-767-1
; Sequence 1, Application US/10497767
; Publication No. US20050261836A1
; GENERAL INFORMATION:
; APPLICANT: VERTEX PHARMACEUTICALS INCORPORATED
; APPLICANT: MENG, WUYI
; APPLICANT: SWENSON, LOVOKA
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF MITOGEN-ACTIVATED PROTEIN
; TITLE OF INVENTION: KINASE-ACTIVATED PROTEIN KINASE 2 AND BINDING POCKETS
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: VPI/01-13 PCT
; CURRENT APPLICATION NUMBER: US/10/497,767
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: 60/337,513
; PRIOR FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 1
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-497-767-1

Query Match          100.0%; Score 2106; DB 5; Length 400;
Best Local Similarity 100.0%; Pred. No. 4.5e-133;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQGSPVPVPPAPAPPQPPTPALPHPPAQPPTPPQPFQFHVKSGLIQKNAIIDDYK 60
Db 5 SQGSPVPVPPAPAPPQPPTPALPHPPAQPPTPPQPFQFHVKSGLIQKNAIIDDYK 64
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Qy 361 VDVEQIKKIKKIEDASNPILLIKRRKKARALEAALAH 396  
Db 365 VDVEQIKKIKKIEDASNPILLIKRRKKARALEAALAH 400

RESULT 7

US-10-081-119-34  
; Sequence 34, Application US/10081119  
; Publication No. US20030045491A1  
; GENERAL INFORMATION:  
; APPLICANT: Reinhard, Christoph  
; APPLICANT: Jefferson, Anne B.  
; APPLICANT: Chan, Vivien W.  
; TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic  
; TITLE OF INVENTION: Target in Cancer  
; FILE REFERENCE: 16932.002  
; CURRENT FILING DATE: 2002-02-21  
; PRIOR APPLICATION NUMBER: US/10/081.119  
; PRIOR APPLICATION NUMBER: 60/289,813  
; PRIOR FILING DATE: 2001-02-21  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 34  
; LENGTH: 370  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-081-119-34

Query Match 89.4%; Score 1882; DB 4; Length 370;  
Best Local Similarity 100.0%; Pred. No. 4.4e-118;  
Matches 349; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 5 SQGSPVPVPPAPAPPQPTPALPHPPAQPFPQFHVKSGLQIKKNAIIDYK 64  
Qy 61 VTSQVLGLGKNGKVLQIFNKRTQEKFKALQKMLQDCKPARRVELHWRASQCPHIVRVDVY 120  
Db 65 VTSQVLGLGKNGKVLQIFNKRTQEKFKALQKMLQDCKPARRVELHWRASQCPHIVRVDVY 124  
Qy 121 ENLYAGRKCLLIWMECLDGGELFSRIQDRGDAQFTEREASEIMKSIGEAIQYLHSINIAH 180  
Db 125 ENLYAGRKCLLIWMECLDGGELFSRIQDRGDAQFTEREASEIMKSIGEAIQYLHSINIAH 184  
Qy 181 RDVKPENLLYTSKRPNAILKLTDFGPAKETTSNLSLTPCYTPYYVAPEVLGPEKDKSC 240  
Db 185 RDVKPENLLYTSKRPNAILKLTDFGPAKETTSNLSLTPCYTPYYVAPEVLGPEKDKSC 244  
Qy 241 DMWSLGVIMYILLCGYPFPFYSNHGLAISPGMKTRIRMGQYEFNPNWSEVSEVKMLRN 300  
Db 245 DMWSLGVIMYILLCGYPFPFYSNHGLAISPGMKTRIRMGQYEFNPNWSEVSEVKMLRN 304  
Qy 301 LLKTEPTQRMITEFNMHPWIMQSTKVPQTPPLHTSRVLKEDKERWEDVK 349  
Db 305 LLKTEPTQRMITEFNMHPWIMQSTKVPQTPPLHTSRVLKEDKERWEDVK 353

RESULT 8

US-10-645-190-2  
; Sequence 2, Application US/10645190  
; Publication No. US20040110710A1  
; GENERAL INFORMATION:  
; APPLICANT: BRISTOL-MYERS SQUIBB COMPANY  
; TITLE OF INVENTION: METHODS FOR PREVENTING ISCHEMIC BRAIN INJURY  
; FILE REFERENCE: D0299 NP  
; CURRENT FILING DATE: 2003-08-21  
; PRIOR APPLICATION NUMBER: US/10/645.190  
; PRIOR FILING DATE: 2002-08-23  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2  
; LENGTH: 370

; TYPE: PRT  
; ORGANISM: Human  
US-10-645-190-2

Query Match 89.4%; Score 1882; DB 4; Length 370;  
Best Local Similarity 100.0%; Pred. No. 4.4e-118;  
Matches 349; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQGSPVPVPPAPAPPQPTPALPHPPAQPFPQFHVKSGLQIKKNAIIDYK 60  
Db 5 SQGSPVPVPPAPAPPQPTPALPHPPAQPFPQFHVKSGLQIKKNAIIDYK 64  
Qy 61 VTSQVLGLGKNGKVLQIFNKRTQEKFKALQKMLQDCKPARRVELHWRASQCPHIVRVDVY 120  
Db 65 VTSQVLGLGKNGKVLQIFNKRTQEKFKALQKMLQDCKPARRVELHWRASQCPHIVRVDVY 124  
Qy 121 ENLYAGRKCLLIWMECLDGGELFSRIQDRGDAQFTEREASEIMKSIGEAIQYLHSINIAH 180  
Db 125 ENLYAGRKCLLIWMECLDGGELFSRIQDRGDAQFTEREASEIMKSIGEAIQYLHSINIAH 184  
Qy 181 RDVKPENLLYTSKRPNAILKLTDFGPAKETTSNLSLTPCYTPYYVAPEVLGPEKDKSC 240  
Db 185 RDVKPENLLYTSKRPNAILKLTDFGPAKETTSNLSLTPCYTPYYVAPEVLGPEKDKSC 244  
Qy 241 DMWSLGVIMYILLCGYPFPFYSNHGLAISPGMKTRIRMGQYEFNPNWSEVSEVKMLRN 300  
Db 245 DMWSLGVIMYILLCGYPFPFYSNHGLAISPGMKTRIRMGQYEFNPNWSEVSEVKMLRN 304  
Qy 301 LLKTEPTQRMITEFNMHPWIMQSTKVPQTPPLHTSRVLKEDKERWEDVK 349  
Db 305 LLKTEPTQRMITEFNMHPWIMQSTKVPQTPPLHTSRVLKEDKERWEDVK 353

Query Match 89.4%; Score 1882; DB 5; Length 370;  
Best Local Similarity 100.0%; Pred. No. 4.4e-118;  
Matches 349; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQGSPVPVPPAPAPPQPTPALPHPPAQPFPQFHVKSGLQIKKNAIIDYK 60  
Db 5 SQGSPVPVPPAPAPPQPTPALPHPPAQPFPQFHVKSGLQIKKNAIIDYK 64  
Qy 61 VTSQVLGLGKNGKVLQIFNKRTQEKFKALQKMLQDCKPARRVELHWRASQCPHIVRVDVY 120  
Db 65 VTSQVLGLGKNGKVLQIFNKRTQEKFKALQKMLQDCKPARRVELHWRASQCPHIVRVDVY 124  
Qy 121 ENLYAGRKCLLIWMECLDGGELFSRIQDRGDAQFTEREASEIMKSIGEAIQYLHSINIAH 180  
Db 125 ENLYAGRKCLLIWMECLDGGELFSRIQDRGDAQFTEREASEIMKSIGEAIQYLHSINIAH 184

QY 181 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSHNSLTTPCYTPYVAPEVLGPEKYDKSC 240  
DB 185 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSHNSLTTPCYTPYVAPEVLGPEKYDKSC 244  
QY 241 DMWSLGVIMYILLCGYPPFYNSHGLAISPGMKTRIRMGQYEFPPNPWSEVSEEVKMLRN 300  
DB 245 DMWSLGVIMYILLCGYPPFYNSHGLAISPGMKTRIRMGQYEFPPNPWSEVSEEVKMLRN 304  
QY 301 LLKTEPTQRTMTITFNMHPWIMQSTKVQTPQLHTSRVLKEDKERWEDVK 349  
DB 305 LLKTEPTQRTMTITFNMHPWIMQSTKVQTPQLHTSRVLKEDKERWEDVK 353

RESULT 10  
US-10-951-406-34  
; Sequence 34, Application US/10951406  
; Publication No. US20050059630A1  
; GENERAL INFORMATION:  
; APPLICANT: Reinhard, Christoph  
; APPLICANT: Jefferson, Anne B.  
; APPLICANT: Chan, Vivien W.  
; TITLE OF INVENTION: TTK in diagnosis and as a Therapeutic  
; FILE REFERENCE: 16932.002  
; CURRENT APPLICATION NUMBER: US/10/951,406  
; CURRENT FILING DATE: 2004-09-27  
; PRIOR APPLICATION NUMBER: US/10/081,119  
; PRIOR FILING DATE: 2002-02-21  
; PRIOR APPLICATION NUMBER: 60/289,813  
; PRIOR FILING DATE: 2001-02-21  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 34  
; LENGTH: 370  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-951-406-34

Query Match 89.4%; Score 1882; DB 5; Length 370;  
Best Local Similarity 100.0%; Pred. No. 4.4e-118;  
Matches 349; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQQSPPVPPFAPAPPQPTPALPHPPAOPPPPPQFPQFHVKSLGQIKKNAIIDYK 60  
DB 5 SQQSPPVPPFAPAPPQPTPALPHPPAOPPPPPQFPQFHVKSLGQIKKNAIIDYK 64  
QY 61 VTSQVLGLGINGKVLQIFNKRTOEKFKALMLQDCPKARREVELHWRASQCPHIVRVDVY 120  
DB 65 VTSQVLGLGINGKVLQIFNKRTOEKFKALMLQDCPKARREVELHWRASQCPHIVRVDVY 124  
QY 121 ENLYAGRKCLLIWECLDGGELFSRIQDRGDAQFTEREASEIMKSIGEAIQYLHSINIAH 180  
DB 125 ENLYAGRKCLLIWECLDGGELFSRIQDRGDAQFTEREASEIMKSIGEAIQYLHSINIAH 184  
QY 181 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSHNSLTTPCYTPYVAPEVLGPEKYDKSC 240  
DB 185 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSHNSLTTPCYTPYVAPEVLGPEKYDKSC 244  
QY 241 DMWSLGVIMYILLCGYPPFYNSHGLAISPGMKTRIRMGQYEFPPNPWSEVSEEVKMLRN 300  
DB 245 DMWSLGVIMYILLCGYPPFYNSHGLAISPGMKTRIRMGQYEFPPNPWSEVSEEVKMLRN 304  
QY 301 LLKTEPTQRTMTITFNMHPWIMQSTKVQTPQLHTSRVLKEDKERWEDVK 349  
DB 305 LLKTEPTQRTMTITFNMHPWIMQSTKVQTPQLHTSRVLKEDKERWEDVK 353

RESULT 11  
US-10-951-477-34  
; Sequence 34, Application US/10951477  
; Publication No. US20050063974A1  
; GENERAL INFORMATION:

; APPLICANT: Reinhard, Christoph  
; APPLICANT: Jefferson, Anne B.  
; APPLICANT: Chan, Vivien W.  
; TITLE OF INVENTION: TTK in diagnosis and as a Therapeutic  
; FILE REFERENCE: 16932.002  
; CURRENT APPLICATION NUMBER: US/10/951,477  
; CURRENT FILING DATE: 2004-09-27  
; PRIOR APPLICATION NUMBER: US/10/081,119  
; PRIOR FILING DATE: 2002-02-21  
; PRIOR APPLICATION NUMBER: 60/289,813  
; PRIOR FILING DATE: 2001-02-21  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 34  
; LENGTH: 370  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-951-477-34

Query Match 89.4%; Score 1882; DB 5; Length 370;  
Best Local Similarity 100.0%; Pred. No. 4.4e-118;  
Matches 349; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQQSPPVPPFAPAPPQPTPALPHPPAOPPPPPQFPQFHVKSLGQIKKNAIIDYK 60  
DB 5 SQQSPPVPPFAPAPPQPTPALPHPPAOPPPPPQFPQFHVKSLGQIKKNAIIDYK 64  
QY 61 VTSQVLGLGINGKVLQIFNKRTOEKFKALMLQDCPKARREVELHWRASQCPHIVRVDVY 120  
DB 65 VTSQVLGLGINGKVLQIFNKRTOEKFKALMLQDCPKARREVELHWRASQCPHIVRVDVY 124  
QY 121 ENLYAGRKCLLIWECLDGGELFSRIQDRGDAQFTEREASEIMKSIGEAIQYLHSINIAH 180  
DB 125 ENLYAGRKCLLIWECLDGGELFSRIQDRGDAQFTEREASEIMKSIGEAIQYLHSINIAH 184  
QY 181 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSHNSLTTPCYTPYVAPEVLGPEKYDKSC 240  
DB 185 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSHNSLTTPCYTPYVAPEVLGPEKYDKSC 244  
QY 241 DMWSLGVIMYILLCGYPPFYNSHGLAISPGMKTRIRMGQYEFPPNPWSEVSEEVKMLRN 300  
DB 245 DMWSLGVIMYILLCGYPPFYNSHGLAISPGMKTRIRMGQYEFPPNPWSEVSEEVKMLRN 304  
QY 301 LLKTEPTQRTMTITFNMHPWIMQSTKVQTPQLHTSRVLKEDKERWEDVK 349  
DB 305 LLKTEPTQRTMTITFNMHPWIMQSTKVQTPQLHTSRVLKEDKERWEDVK 353

RESULT 12  
US-10-977-087-34  
; Sequence 34, Application US/10977087  
; Publication No. US20050130926A1  
; GENERAL INFORMATION:  
; APPLICANT: Reinhard, Christoph  
; APPLICANT: Jefferson, Anne B.  
; APPLICANT: Chan, Vivien W.  
; APPLICANT: Kaufmann, Joerg  
; APPLICANT: Xin, Hong  
; APPLICANT: Kennedy, Giulia C.  
; APPLICANT: Khoja, Hamiduddin  
; APPLICANT: Shyamala, Venkatakrishna  
; TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED IN CANCEROUS CELLS  
; FILE REFERENCE: 2300-21986  
; CURRENT APPLICATION NUMBER: US/10/977,087  
; CURRENT FILING DATE: 2004-10-28  
; PRIOR APPLICATION NUMBER: 10/081,119  
; PRIOR FILING DATE: 2002-02-21  
; PRIOR APPLICATION NUMBER: 60/271,254  
; PRIOR FILING DATE: 2001-02-21  
; PRIOR APPLICATION NUMBER: 10/360,848  
; PRIOR FILING DATE: 2003-02-06

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; PRIOR APPLICATION NUMBER: 09/570,593
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: 60/134,112
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 10/763,692
; PRIOR FILING DATE: 2004-01-22
; PRIOR APPLICATION NUMBER: 09/626,301
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: 60/148,936
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/145,612
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: 10/698,959
; PRIOR FILING DATE: 2003-10-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-977-087-34

Query Match      89.4%; Score 1882; DB 5; Length 370;
Best Local Similarity 100.0%; Pred. No. 4.4e-118; Indels 0; Gaps 0;
Matches 349; Conservative 0; Mismatches 0;

Qy 1 SQGSPVPVPAPAPPQPPPTPALPHPPAQQPPPPPPQFPQFHVKSGLQIKKNAIIDDYK 60
Db 5 SQGSPVPVPAPAPPQPPPTPALPHPPAQQPPPPPPQFPQFHVKSGLQIKKNAIIDDYK 64
Qy 61 VTSQVLGLGKNGVLQIFNKRTOEKFAKMLQDCPKARREVELHWRASQCPHIVRVDVY 120
Db 65 VTSQVLGLGKNGVLQIFNKRTOEKFAKMLQDCPKARREVELHWRASQCPHIVRVDVY 124
Qy 121 ENLYAGRKCLLIWMECLDGGELFSRIQDRGDOAFTEREASEIMKSGIQAIOYLHNSINIAH 180
Db 125 ENLYAGRKCLLIWMECLDGGELFSRIQDRGDOAFTEREASEIMKSGIQAIOYLHNSINIAH 184
Qy 181 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSNLSLTPCYTPYYVAPEVLGPEKYDKSC 240
Db 185 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSNLSLTPCYTPYYVAPEVLGPEKYDKSC 244
Qy 241 DMWSLGVIMVILLGYPFYSNHGLAISPGMKTRIRMGQYEFPPNPSEVSEVKMLIRN 300
Db 245 DMWSLGVIMVILLGYPFYSNHGLAISPGMKTRIRMGQYEFPPNPSEVSEVKMLIRN 304
Qy 301 LLKTEPTQRMITTEFMNHPIMQSTKVPQTPPLHTSRVLKEDKERWEDVK 349
Db 305 LLKTEPTQRMITTEFMNHPIMQSTKVPQTPPLHTSRVLKEDKERWEDVK 353

RESULT 13
US-10-664-421-114
; Sequence 114, Application US/10664421
; Publication No. US20040142864A1
; GENERAL INFORMATION:
; APPLICANT: BREMER, RYAN
; APPLICANT: IBRAHIM, PRABHA
; APPLICANT: KUMAR, ABHINAV
; APPLICANT: MANDIYAN, VALSAN
; APPLICANT: MILBURN, MICHAEL V.
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
; FILE REFERENCE: 039363/0703
; CURRENT APPLICATION NUMBER: US/10/664,421
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/412,341
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/411,398
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 114

; PRIOR APPLICATION NUMBER: 09/570,593
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: 60/134,112
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 10/763,692
; PRIOR FILING DATE: 2004-01-22
; PRIOR APPLICATION NUMBER: 09/626,301
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: 60/148,936
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/145,612
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: 10/698,959
; PRIOR FILING DATE: 2003-10-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-977-087-34

Query Match      89.4%; Score 1882; DB 5; Length 370;
Best Local Similarity 100.0%; Pred. No. 4.4e-118; Indels 0; Gaps 0;
Matches 349; Conservative 0; Mismatches 0;

Qy 1 SQGSPVPVPAPAPPQPPPTPALPHPPAQQPPPPPPQFPQFHVKSGLQIKKNAIIDDYK 60
Db 5 SQGSPVPVPAPAPPQPPPTPALPHPPAQQPPPPPPQFPQFHVKSGLQIKKNAIIDDYK 64
Qy 61 VTSQVLGLGKNGVLQIFNKRTOEKFAKMLQDCPKARREVELHWRASQCPHIVRVDVY 120
Db 65 VTSQVLGLGKNGVLQIFNKRTOEKFAKMLQDCPKARREVELHWRASQCPHIVRVDVY 124
Qy 121 ENLYAGRKCLLIWMECLDGGELFSRIQDRGDOAFTEREASEIMKSGIQAIOYLHNSINIAH 180
Db 125 ENLYAGRKCLLIWMECLDGGELFSRIQDRGDOAFTEREASEIMKSGIQAIOYLHNSINIAH 184
Qy 181 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSNLSLTPCYTPYYVAPEVLGPEKYDKSC 240
Db 185 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSNLSLTPCYTPYYVAPEVLGPEKYDKSC 244
Qy 241 DMWSLGVIMVILLGYPFYSNHGLAISPGMKTRIRMGQYEFPPNPSEVSEVKMLIRN 300
Db 245 DMWSLGVIMVILLGYPFYSNHGLAISPGMKTRIRMGQYEFPPNPSEVSEVKMLIRN 304
Qy 301 LLKTEPTQRMITTEFMNHPIMQSTKVPQTPPLHTSRVLKEDKERWEDVK 349
Db 305 LLKTEPTQRMITTEFMNHPIMQSTKVPQTPPLHTSRVLKEDKERWEDVK 353

RESULT 14
US-10-941-635-115
; Sequence 115, Application US/10941635
; Publication No. US20050164300A1
; GENERAL INFORMATION:
; APPLICANT: ARTIS, DEAN R.
; APPLICANT: BREMER, RYAN E.
; APPLICANT: GILLETTE, SAMUEL J.
; APPLICANT: HURT, CLARENCE R.
; APPLICANT: IBRAHIM, PRABHA L.
; APPLICANT: ZUCKERMAN, REBECCA L.
; TITLE OF INVENTION: MOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVELOPMENT
; FILE REFERENCE: 039363-1702
; CURRENT APPLICATION NUMBER: US/10/941,635
; CURRENT FILING DATE: 2004-09-15
; PRIOR APPLICATION NUMBER: 60/503,277
; PRIOR FILING DATE: 2003-09-15
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 115
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Mammalian
; OTHER INFORMATION: protein sequence
US-10-941-635-115

Query Match      87.0%; Score 1833; DB 5; Length 357;
Best Local Similarity 100.0%; Pred. No. 8.1e-115; Indels 0; Gaps 0;
Matches 340; Conservative 0; Mismatches 0;

Qy 10 FPAPAPPQPPTPALPHPPAQQPPPPPPQFPQFHVKSGLQIKKNAIIDDYKVTQSQVLGLG 69
Db 1 FPAPAPPQPPTPALPHPPAQQPPPPPPQFPQFHVKSGLQIKKNAIIDDYKVTQSQVLGLG 60
Qy 70 INKVLQIFNKRTOEKFAKMLQDCPKARREVELHWRASQCPHIVRVDVYENLYAGRK 129
Db 61 INKVLQIFNKRTOEKFAKMLQDCPKARREVELHWRASQCPHIVRVDVYENLYAGRK 120
Qy 130 LLIVMECLDGGELFSRIQDRGDOAFTEREASEIMKSGIQAIOYLHNSINIAHRAHVDKPENLL 189
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Qy 250 YLLCGYPFYSNHGLAISPGMKTRIRMGQYEFPPNPSEVSEVKMLIRNLLKTEPTQ 309
Db 241 YLLCGYPFYSNHGLAISPGMKTRIRMGQYEFPPNPSEVSEVKMLIRNLLKTEPTQ 300
Qy 310 MTITEFMNHPIMQSTKVPQTPPLHTSRVLKEDKERWEDVK 349
Db 301 MTITEFMNHPIMQSTKVPQTPPLHTSRVLKEDKERWEDVK 340

US-10-941-635-115
; Sequence 115, Application US/10941635
; Publication No. US20050164300A1
; GENERAL INFORMATION:
; APPLICANT: ARTIS, DEAN R.
; APPLICANT: BREMER, RYAN E.
; APPLICANT: GILLETTE, SAMUEL J.
; APPLICANT: HURT, CLARENCE R.
; APPLICANT: IBRAHIM, PRABHA L.
; APPLICANT: ZUCKERMAN, REBECCA L.
; TITLE OF INVENTION: MOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVELOPMENT
; FILE REFERENCE: 039363-1702
; CURRENT APPLICATION NUMBER: US/10/941,635
; CURRENT FILING DATE: 2004-09-15
; PRIOR APPLICATION NUMBER: 60/503,277
; PRIOR FILING DATE: 2003-09-15
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 115
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Mammalian
; OTHER INFORMATION: protein sequence
US-10-941-635-115

Query Match      87.0%; Score 1833; DB 5; Length 357;
Best Local Similarity 100.0%; Pred. No. 8.1e-115; Indels 0; Gaps 0;
Matches 340; Conservative 0; Mismatches 0;

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Qy 70 INKVLQIFNKRTOEKFAKMLQDCPKARREVELHWRASQCPHIVRVDVYENLYAGRK 129
Db 61 INKVLQIFNKRTOEKFAKMLQDCPKARREVELHWRASQCPHIVRVDVYENLYAGRK 120
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Qy 130 LLIVMECLDGELFSRIODRGDQAFTEREASEIMKSGEAIQYLHSINIAHRDVKPENLL 189
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Db 181 YTSKRPNAILKLTDFGFAKETTSNLSLTPCYTPYVAPEVLGPEKYDKSCDMSLGVIM 240
Qy 250 YILLCGYPPFFYSNHCGLAISPGMKTRIRMGQYEFEPNPEWSEVSEVKMLIRNLLKTEPTQR 309
Db 241 YILLCGYPPFFYSNHCGLAISPGMKTRIRMGQYEFEPNPEWSEVSEVKMLIRNLLKTEPTQR 300
Qy 310 MTITEFMNHPWIMOSTKVPQTPHLTSHRSVLKEDKERWEDVK 349
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RESULT 15
US-10-116-649-2
; Sequence 2, Application US/10116649
; Publication No. US20040005686A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia
; APPLICANT: Kurumbail, Ravi G
; APPLICANT: Pawlitz, Jennifer L
; APPLICANT: Stegeman, Roderick A
; APPLICANT: Stallings, William C
; APPLICANT: Shieh, Huey S
; APPLICANT: Mourey, Robert J
; APPLICANT: Bolten, Suzanne L
; APPLICANT: Broadus, Richard M
; TITLE OF INVENTION: CRYSTALLINE STRUCTURE OF HUMAN MAPKAP Kinase-2
; FILE REFERENCE: PHA 4184.1
; CURRENT APPLICATION NUMBER: US/10/116.649
; CURRENT FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-649-2

Query Match 82.1%; Score 1729; DB 4; Length 327;
Best Local Similarity 100.0%; Pred. No. 6.9e-108; Mismatches 0; Indels 0; Gaps 0;
Matches 327; Conservative 0;

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Db 1 QFHVKSGLIQKKNAIIDDYKVTQVLGGLGKVLQIFNKRTQKFKALKMLQDCPKARRE 60
Qy 101 VELHWRASQCPIHVIIVDVYENLYAGRKCLLI VMECLDGGELFSRIODRGDQAFTEREAS 160
Db 61 VELHWRASQCPIHVIIVDVYENLYAGRKCLLI VMECLDGGELFSRIODRGDQAFTEREAS 120
Qy 161 EIMKSGEAIQYLHSINIAHRDVKPENLLYTSKRPNALKLTDFGFAKETTSNLSLTPC 220
Db 121 EIMKSGEAIQYLHSINIAHRDVKPENLLYTSKRPNALKLTDFGFAKETTSNLSLTPC 180
Qy 221 YTPYVAPEVLGPEKYDKSCDMSLGVIMYILLCGYPPFFYSNHCGLAISPGMKTRIRMGQY 280
Db 181 YTPYVAPEVLGPEKYDKSCDMSLGVIMYILLCGYPPFFYSNHCGLAISPGMKTRIRMGQY 240
Qy 281 EFPNPEWSEVSEVKMLIRNLLKTEPTQRTWITITEFMNHPWIMOSTKVPQTPHLTSHRSVLKE 340
Db 241 EFPNPEWSEVSEVKMLIRNLLKTEPTQRTWITITEFMNHPWIMOSTKVPQTPHLTSHRSVLKE 300
Qy 341 DKERWEDVKEMTSALATMRVDYEQIK 367
Db 301 DKERWEDVKEMTSALATMRVDYEQIK 327
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GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: June 19, 2006, 09:12:32 ; Search time 23 Seconds  
(without alignments)  
388.366 Million cell updates/sec

Title: US-10-469-221-2

Perfect score: 2106

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 96747 seqs, 22556637 residues

Total number of hits satisfying chosen parameters: 96747

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications AA New:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US09\_NEW\_PUB.pap.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US06\_NEW\_PUB.pap.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US07\_NEW\_PUB.pap.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US08\_NEW\_PUB.pap.\*
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- 6: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US10\_NEW\_PUB.pap.\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US11\_NEW\_PUB.pap.\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US60\_NEW\_PUB.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2106	100.0	400	7	US-11-273-567-4
2	1882	89.4	370	7	US-11-273-567-3
3	1391	66.0	382	6	US-10-505-928-625
4	508.5	24.1	542	6	US-10-449-902-48403
5	487.5	23.1	473	7	US-11-242-505A-42
6	483	22.9	623	6	US-10-449-902-50362
7	475.5	22.6	733	6	US-10-505-928-349
8	474.5	22.5	513	6	US-10-449-902-55199
9	452	21.5	574	6	US-10-449-902-36211
10	435.5	20.7	766	7	US-11-312-958-34
11	434	20.6	588	6	US-10-449-902-46406
12	434	20.6	729	7	US-11-312-958-64
13	433	20.6	533	6	US-10-449-902-47361
14	429.5	20.4	538	6	US-10-449-902-44533
15	428	20.3	459	6	US-10-953-349-906
16	428	20.3	529	6	US-10-953-349-905
17	428	20.3	543	6	US-10-953-349-904
18	427.5	20.3	533	6	US-10-449-902-52316
19	426	20.2	550	6	US-10-449-902-46303
20	426	20.2	563	6	US-10-449-902-51194
21	425	20.2	547	6	US-10-449-902-54833
22	414.5	19.7	542	6	US-10-449-902-44416
23	410.5	19.5	551	6	US-10-449-902-33055
24	404	19.2	527	6	US-10-449-902-44411
25	402	19.1	508	6	US-10-449-902-47145

#### ALIGNMENTS

##### RESULT 1

US-11-273-567-4

; Sequence 4, Application US/11273567

; Publication No. US20060115453A1

; GENERAL INFORMATION:

; APPLICANT: Yaffe, Michael B.

; APPLICANT: Manke, Isaac A.

; APPLICANT: Reinhardt, Hans Christian

; APPLICANT: Lim, Daniel

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING CELLULAR PROLIFERATIVE

; TITLE OF INVENTION: DISEASES

; FILE REFERENCE: 01997/557002

; CURRENT APPLICATION NUMBER: US/11/273,567

; CURRENT FILING DATE: 2005-11-14

; PRIOR APPLICATION NUMBER: 60/627,352

; PRIOR FILING DATE: 2004-11-12

; NUMBER OF SEQ ID NOS: 84

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 4

; LENGTH: 400

; TYPE: PRT

; ORGANISM: Homo sapien

; US-11-273-567-4

Query Match 100.0%; Score 2106; DB 7; Length 400;

Best Local Similarity 100.0%; Pred. No. 3e-96;

Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQSQSPVPFPAPAPPQPPPTPALPHPPAQQPPPPPPQPPQFHVKSLQIKKNAIDDK 60

Db 5 SQSQSPVPFPAPAPPQPPPTPALPHPPAQQPPPPPPQPPQFHVKSLQIKKNAIDDK 64

Qy 61 VTSQVLGLGNGKVLQIENKRTQEKFKALMQLQPCPKARREVELHWRASQCPHIVRIVDVY 120

Db 65 VTSQVLGLGNGKVLQIENKRTQEKFKALMQLQPCPKARREVELHWRASQCPHIVRIVDVY 124

Qy 121 ENLYAGRKCLLIWVECLDGGELFSRIQDRGQDAFTREASEIMKSGEATQYLHSHINIAH 180

Db 125 ENLYAGRKCLLIWVECLDGGELFSRIQDRGQDAFTREASEIMKSGEATQYLHSHINIAH 184

Qy 181 RDVKNENLYTSKRPNAILKLTDFGPAKETTSNSLTTPCYTPYYVAPEVLGPEKDKSC 240

Db 185 RDVKNENLYTSKRPNAILKLTDFGPAKETTSNSLTTPCYTPYYVAPEVLGPEKDKSC 244

Qy 241 DMWSLGVIMYILLCGYPPFYSNHGLAISPMKTRIMSGQVEFFPNPWSVSEVSKMLRN 300

Db 245 DMWSLGVIMYILLCGYPPFYSNHGLAISPMKTRIMSGQVEFFPNPWSVSEVSKMLRN 304

Sequence 4, Appli  
Sequence 36, Appl  
Sequence 4354, A  
Sequence 32014, A  
Sequence 32452, A  
Sequence 53780, A  
Sequence 10927, A  
Sequence 845, App  
Sequence 48594, A  
Sequence 49041, A  
Sequence 56186, A  
Sequence 658, App  
Sequence 38177, A  
Sequence 56570, A  
Sequence 649, App  
Sequence 31553, A  
Sequence 45910, A  
Sequence 43487, A  
Sequence 45088, A  
Sequence 49645, A

26 397 18.9 608 7 US-11-312-958-4  
27 397 18.9 655 7 US-11-312-958-36  
28 391.5 18.6 534 6 US-10-449-902-43354  
29 379.5 18.0 456 6 US-10-449-902-32014  
30 379.5 18.0 456 6 US-10-449-902-32452  
31 379.5 18.0 456 6 US-10-449-902-53780  
32 374.5 17.8 372 6 US-10-953-349-10927  
33 374.5 17.8 431 6 US-10-505-928-845  
34 373 17.7 516 6 US-10-449-902-48594  
35 372 17.7 339 6 US-10-449-902-49041  
36 370 17.6 565 6 US-10-449-902-56186  
37 368 17.5 351 6 US-10-505-928-658  
38 365 17.3 466 6 US-10-449-902-38177  
39 363 17.2 334 6 US-10-449-902-56570  
40 362.5 17.2 435 6 US-10-953-349-649  
41 358 17.0 342 6 US-10-449-902-31553  
42 358 17.0 342 6 US-10-449-902-46910  
43 357.5 17.0 461 6 US-10-449-902-43487  
44 357 17.0 520 6 US-10-449-902-45088  
45 356.5 16.9 461 6 US-10-449-902-49645



Db 15 SQSQSPSPHHKHHHHTTRAPKPKPQPPPP--QQPRSQPPPPRHQPPQAPQAAAA 72  
QY 46 SGLQIKKNAIDDDYKVT--SOVLGLGNGKVLQIFNKRTOEKFKALKWL-----QDC 94  
Db 73 DGVRLVGRPMEDVRATYTTGRELGRGQFGVYIATHKPTGRRYACKSIAARKLARPDLL 132  
QY 95 PKARREVELHWRASQCCHIVIRVDVYENLYAGRKCLLIVMECLDGGELFSGRIODRGDQAF 154  
Db 133 DDVREVEHIMHHLTGHRIIVELRGAYED---RHSVNLVMECLCEGGEFDRILITARGH--Y 186  
QY 155 TEREASIMKSIGEAIOYLHSINIAHRDVKPENLLYTSKRPNAIKLITDFG---FAKETT 211  
Db 187 SERAAAALCREIVSVHSHCSMGVWHRDLKPFENFLNKRDESDPLKATDFGLSVFFKPG 246  
QY 212 SHNSLTTPCYTPYVVAPEVLGPEKYDKSCDMWSIGVIMYILLCGYPPFYSNHGLAISP 271  
Db 247 QFRDLVG---SAYVVAPEVL--KRYLGABADIWSAGVILYILLSGVPPFWAEN----EDGI 298  
QY 272 KTRIRMGQYFPNPENWSEVEVKMLIRNLLKTEPTQRTMTITEPMNHPIWQSTKVPQTP 331  
Db 299 FDAVLQGHIDFSSEPPWFSISSGAKDLVKRMLRQDPKERLTAAETILNHPWIREDEGAPDKP 358  
QY 332 L 332  
Db 359 L 359  
RESULT 5  
US-11-242-505A-42  
; Sequence 42, Application US/11242505A  
; Publication No. US20060099656A1  
; GENERAL INFORMATION:  
; APPLICANT: Carroll, Joseph M.  
; APPLICANT: Healy, Aileen  
; TITLE OF INVENTION: Methods and Compositions for Treating  
; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,  
; FILE OF INVENTION: 14395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310,  
; FILE REFERENCE: MPI2001-288PIRCP1OWNIM  
; CURRENT APPLICATION NUMBER: US/11/242,505A  
; CURRENT FILING DATE: 2005-10-03  
; PRIOR APPLICATION NUMBER: US 10/290,078  
; PRIOR FILING DATE: 2002-11-07  
; PRIOR APPLICATION NUMBER: US 60/347,949  
; PRIOR FILING DATE: 2001-11-07  
; PRIOR APPLICATION NUMBER: US 10/320,351  
; PRIOR FILING DATE: 2002-12-16  
; PRIOR APPLICATION NUMBER: 60/341,606  
; PRIOR FILING DATE: 2001-12-17  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 42  
; LENGTH: 473  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-242-505A-42  
Query Match 23.1%; Score 487.5; DB 7; Length 473;  
Best Local Similarity 37.5%; Pred. No. 1.6e-17;  
Matches 111; Conservative 55; Mismatches 113; Indels 17; Gaps 7;  
QY 29 AQPDPDPDPQPPQPPHVKSGSLQIKKNAIDDDYKVTQSVGLGNGKVLQIFNKRTOEKFKAL 88  
Db 19 ASAAPGTASLVDPYDWIGDS---NRDALSDFFEVESE-LGRGATSVYVRCKQKQTPYAL 74  
QY 89 KMLQ---DCPKARREVELHWRASQCCHIVIRVDVYENLYAGRKCLLIVMECLDGGELF 145  
Db 75 KVLKKTVDKXIVRTEIGVLLRLSH-PNIIKKEIFETPTT-----ISLVLELVTTGGELFDR 129  
QY 146 IODRGDQAFTEREASEIMKSIGEAIOYLHSINIAHRDVKPENLLYTSKRPNAIKLITDFG 205  
Db 130 IVEKG--YYSERDAADAVKQILBAVYLVHNGVIVHRDLKPFENLLYATPAPDAPEKLTADF 187  
QY 206 FAKETTSHNSLTTPCYTPYVVAPEVLGPEKYDKSCDMWSIGVIMYILLCGYPPFYSNHGL 265

Db 188 LSKIVEHQLMKTVCGTGPGYCAPELLRGCAYPGEVDMWSVGIIYILLCGFEFPYDERG- 246  
QY 266 AISPQMKTRIRMGQYFPNPENWSEVEVKMLIRNLLKTEPTQRTMTITEPMNHPIW 321  
Db 247 --DQFMFRILNCEYFISPWDEVSINAKDLVRKLIIVLDPKKRLTTFQALQHPWV 300  
RESULT 6  
US-10-449-902-50362  
; Sequence 50362, Application US/10449902  
; Publication No. US20060123505A1  
; GENERAL INFORMATION:  
; APPLICANT: National Institute of Agrobiological Sciences.  
; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
; APPLICANT: The Institute of Physical and Chemical Research.  
; APPLICANT: Foundation for Advancement of International Science.  
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF  
; FILE REFERENCE: MOA-A0205Y1-US  
; CURRENT APPLICATION NUMBER: US/10/449,902  
; CURRENT FILING DATE: 2003-05-29  
; PRIOR APPLICATION NUMBER: JP 2002-203269  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: JP 2002-383870  
; NUMBER OF SEQ ID NOS: 56791  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 50362  
; LENGTH: 623  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
US-10-449-902-50362  
Query Match 22.9%; Score 483; DB 6; Length 623;  
Best Local Similarity 29.8%; Pred. No. 3.3e-17;  
Matches 128; Conservative 68; Mismatches 148; Indels 88; Gaps 13;  
QY 13 PAPPPOPPPALPHPPPAQPPPP-----PPPOQFP 40  
Db 50 PAPP--PPTSDAPLAVQNKPPPEHVKIVSTDTASARQDASKSSAGSDSGEAARPRVPP 107  
QY 41 QPHVKS-----LQIKKNAIDDDYKVTQSVGLGNGKVLQIFNKRTOEKFKALKML-- 91  
Db 108 VKRVSSAGLLVGSVLKRRKTESLKDKVSL-GRKLGQCGFTTYLCVERATGKEFACKSILK 166  
QY 92 -----QDCPKARREVELHWRASQCCHIVIRVDVYENLYAGRKCLLIVMECLDGGELF 145  
Db 167 RKLVTDDDDVEDVRREIQIMYHLGHNVISIRGAYEDAVA-----VHLVMECLAGGELFDR 222  
QY 146 IODRGDQAFTEREASEIMKSIGEAIOYLHSINIAHRDVKPENLLYTSKRPNAIKLITDFG 205  
Db 223 IVOKGH--YTERKAELARVIVGVVCHSMGVWHRDLKPFENLFDQOTEAAALKITIDFG 280  
QY 206 FAKETTSHNSLTTPCYTPYVVAPEVLGPEKYDKSCDMWSIGVIMYILLCGYPPFYSNHGL 265  
Db 281 LSIFRPPQGVFTDVGSPYVVAPEVL-KKKYQGEADVWSAGVILYILLCGVPPFWAEN-- 337  
QY 266 AISPQMKTRIRMGQYFPNPENWSEVEVKMLIRNLLKTEPTQRTMTITEPMNHPIWQST 325  
Db 338 --EQGFEFVHLGRDLFQSEPPWPSISEGAKDLVRMLVRDPKKRLTAHEVLRHPWVQVGG 395  
QY 326 KVPQTEPLHTSRVLKEDKE-----RWEDVKEEMTSALATM-----RV 361  
Db 396 LAPDKEL-DSAVLSRNKQFSAMNKLKMAIRVIAENLSEDEIAGLKEMFKMIDTDSGOI 454  
QY 362 DYEQIKI--KKI 371  
Db 455 TFEELKVLKXV 466  
RESULT 7  
US-10-505-928-349  
; Sequence 349, Application US/10505928

```
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 349
; LENGTH: 733
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-349

Query Match      22.6%; Score 475.5; DB 6; Length 733;
Best Local Similarity 32.8%; Pred. No. 8.9e-17;
Matches 113; Conservative 66; Mismatches 111; Indels 55; Gaps 12;

QY 10 FPAPAPPPQPPTP-----ALPHPPAQ-----PPPPPPQPF--PQFHV 44
DB 352 FTARTDTSQVPPSANAHHLFRGSFVASSLIQEPSQDLHKVPVHPVIVQQLHGNNHF 411
QY 45 KSGLIQKNAIDDYKVTOSVGLGKINGKVLQIFNKRTOBKFKMLQDCPKARR-----E 100
DB 412 TDGYEIKEDIGVGSYCKRCV-----HKATDTEYAVKIID---KSKRDPSEE 456
QY 101 VELHWRASQCPHVRIVDVYENLYAGRKCLLIWMECLDGGELFSRIODRGDQAFTEREAS 160
DB 457 IEILLRYGQHPNIITIKDVYDD---GKFVYLWELMRGEGELDLRIHQ--RYFSREAS 510
QY 161 EIMKSICEATQYLSHINIAHRDVKPNLLY--TSKRPNAIKLTDFGFAKETTSHNS-LT 217
DB 511 DVLCTITKMDYLSQGVVHRDLKPSNLYRDESGSPESI-RVCDGFGAKQLRAGNGLLM 569
QY 218 TPCYTPYVAPEVLGPEKDYKSCDMSLGVIMVILLCGYPPFYSNHNGLAISPGMKTRIRM 277
DB 570 TPCYTANFAPEVLKRGYDAACDIWSLGILLYTMLAGFTPF-ANGPDDTPEBILARIGS 628
QY 278 GQYEFNPESEVSEEVKMLIRNLKTEPTORMTITEFNMHPWIM 322
DB 629 GKVALSGNWDSSDAAKOVVSKMLHVDHPHQRUTAMQVLKHPWV 673

RESULT 8
US-10-449-902-55199
; Sequence 55199, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55199
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-55199

Query Match      22.5%; Score 474.5; DB 6; Length 513;
Best Local Similarity 33.3%; Pred. No. 7.3e-17;

Matches 113; Conservative 56; Mismatches 113; Indels 57; Gaps 8;

QY 14 APPQPQ-----PTPALPHPPAQPPPPPPQPFQFHVKSLQIKKNAIDDYKVTOSVGL 68
DB 21 APPPVTAAGGRPVSVLP-----KTNVVRDHYRIGKKG 55
QY 69 GINGKVLQIFNKRTOBKFKML-----ODCPKARREVELHWRASQCPHVRIVDVY 120
DB 56 GQFGTTLVCLVDKASGGEFACKSIKPKLLCREDEYDVMREIQIMHLSHPNVVIRGAY 115
QY 121 ENLYAGRKCLLIWMECLDGGELFSRIODRGDQAFTEREASEIMKSGEAIQYLSHINIAH 180
DB 116 EDAL-----FVHIVMELCAGGELFDRIVAKGH--YTERAAAQLIRTIIVAVVEGCHSLGVMH 169
QY 181 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSHNSLTTPCYTPYVAPEVL-----GPEKY 236
DB 170 RDLKPENFLFASAAEDAPLKATDFGLSMFYKPGDKPSDVVGSPYVAPEVLQKCYGPES- 228
QY 237 DKSCDMSLGVIMVILLCGYPPFYSNHNGLAISPGMKTRIRMGOYEFNPESEVSEVKM 296
DB 229 ----DVMSAGVILYILLCGVPPFWAB-----TEAGIFRQILRGKLDPESEFWPSPISDSAKD 280
QY 297 LIRNLKTEPTORMTITEFNMHPWIMQSTKVQPTPLHTS 335
DB 281 LVNMLCRDPTKRLTAHEVLCHPWIVDDAVADPKPDSA 319

RESULT 9
US-10-449-902-36211
; Sequence 36211, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36211
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-36211

Query Match      21.5%; Score 452; DB 6; Length 574;
Best Local Similarity 31.4%; Pred. No. 1e-15;
Matches 120; Conservative 62; Mismatches 154; Indels 46; Gaps 12;

QY 13 PAPPQPPTPALPHPPAQPPPPPPQPF-----QFHVKSCL--QIKKNAIDDYKVT 62
DB 48 PKPKPKPRARAKPNPYDW---APPRVLPARGGAASAVRLEGVPHHPHRLRVTDKYQL- 103
QY 63 SOVLGLGKINGKVLQIFNKRTOBKFKMLQ-----DCPKARREVELHWRASQCPHIV 114
DB 104 GRELGGEFGVTHLATDRATRELACKSIKPKRLRTADVADVVRREVAIMASLPDHPALV 163
QY 115 RIVDVYENLYAGRKCLLIWMECLDGGELFSRIODRGDQAFTEREASEIMKSIGEATQYLSH 174
DB 164 ELRAAYEDADA-----VHLWELCDGGELFDRIVARG--RYTERAAAAAARTVAEVVRACH 217
QY 175 SINIAHRDVKPNLLYTSKRPNAILKLTDFGFAKETTSHNSLTTPCYTPYVAPEVL--- 231
DB 218 AHGVMHRDLKPNFLYAGKAEDAQLKAIDFGLSVFFRPGERFREIVGSPYMAPEVLRRD 277
QY 232 -GPEKYDKSCDMSLGVIMVILLCGYPPFYSNHNGLAISPGMKTRIRMGOYEFNPESEV 290
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Db 441 AN---LKSEITLMEAA 455

RESULT 12

US-11-312-958-64

; Sequence 64, Application US/11312958

; Publication No. US20060100152A1

; GENERAL INFORMATION:

; APPLICANT: Millennium Pharmaceuticals, Inc.

; APPLICANT: Rosenfeld, Julie Beth

; APPLICANT: Silos-Santiago, Immaculada

; TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING

; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 9949, 14230, 760, 62553,

; TITLE OF INVENTION: 12216, 17719, 41897, 47174, 33408, 10002, 16209, 314, 636,

; TITLE OF INVENTION: 27410, 33260, 619, 15985, 69112, 2158, 224, 615, 44373,

; TITLE OF INVENTION: 95431, 22245, 2387, 16658, 55054, 16314, 1613, 1675, 9569 OR

; TITLE OF INVENTION: 13424 MOLECULES

; FILE REFERENCE: MPI02-027PIRNOWNIM

; CURRENT APPLICATION NUMBER: US/11/312,958

; CURRENT FILING DATE: 2005-12-20

; PRIOR APPLICATION NUMBER: US/10/369,022

; PRIOR FILING DATE: 2003-02-19

; PRIOR APPLICATION NUMBER: US 60/360,495

; PRIOR FILING DATE: 2002-02-28

; PRIOR APPLICATION NUMBER: US 60/370,121

; PRIOR FILING DATE: 2002-04-04

; PRIOR APPLICATION NUMBER: US 60/373,010

; PRIOR FILING DATE: 2002-04-16

; PRIOR APPLICATION NUMBER: US 60/373,908

; PRIOR FILING DATE: 2002-04-19

; PRIOR APPLICATION NUMBER: US 60/377,717

; PRIOR FILING DATE: 2002-05-03

; PRIOR APPLICATION NUMBER: US 60/379,949

; PRIOR FILING DATE: 2002-05-13

; PRIOR APPLICATION NUMBER: US 60/382,409

; PRIOR FILING DATE: 2002-05-21

; PRIOR APPLICATION NUMBER: US 60/385,280

; PRIOR FILING DATE: 2002-06-03

; PRIOR APPLICATION NUMBER: US 60/386,879

; PRIOR FILING DATE: 2002-06-06

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 64

; LENGTH: 729

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-312-958-64

Query Match 20.6%; Score 434; DB 7; Length 729;

Best Local Similarity 37.5%; Pred. No. 9.2e-15;

Matches 110; Conservative 46; Mismatches 99; Indels 38; Gaps 12;

Qy 45 KSLQIKKNAIDDKYKTSQVLGGLGKGVQIFNKRKTQEKFKALMLQDCPKAR----- 98

Db 377 EEGQIPA-TITERYKV-GRITGDNFVAVKCEVERSTARAYALKIKK-SKCRGKHEMI 433

Qy 99 -REVELHWRASQCPHIVRIV---DVYENLYAGRKCLLIVMECLDGGELFSRIQDRGQDAF 154

Db 434 QNEVSIILRRVKH-PNIVILLIEMDVPTELY-----LVNELVKGGLDFDAI--TSTNKY 483

Qy 155 TERASEIMKSGIAIOYLSINIAHRRDVKPENLL-YTSKRPNAILKLITDFGFAKETTS 213

Db 484 TERDASGMYNLASAICYLHSLNIVHRDIKPENLLVVEHQDGSKSLKLGDFGLA--TIVD 541

Qy 214 NSLTPCCTPYVAPEVLGPEKYDKSCDMSLGVIMVILCGYPPFVSNHGLAISPG--- 270

Db 542 GPLTVCGCTPYVAPEIIAETGYGLKVDIWAAGVITYILLCGFPFPRGS-----GDDQ 594

Qy 271 --MKTRIRMGQYEPNPENSWSEVSKMLIRNLKTEPTQRTMTITERMHPWI 321

Db 595 EVBFDQILMGQDFPSPYDWNVDSAKELITMMLLVDDVDQRFSAVOVLEHPWV 647

RESULT 13

US-10-449-902-47361

; Sequence 47361, Application US/10449902

; Publication No. US20060123505A1

; GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences, Institution.

; APPLICANT: Bio-oriented Technology Research Advancement

; APPLICANT: The Institute of Physical and Chemical Research.

; APPLICANT: Foundation for Advancement of International Science.

; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF

; FILE REFERENCE: MOA-A0205Y1-US

; CURRENT APPLICATION NUMBER: US/10/449,902

; CURRENT FILING DATE: 2003-05-29

; PRIOR APPLICATION NUMBER: JP 2002-203269

; PRIOR FILING DATE: 2002-05-30

; PRIOR APPLICATION NUMBER: JP 2002-383870

; PRIOR FILING DATE: 2002-12-11

; NUMBER OF SEQ ID NOS: 56791

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 47361

; LENGTH: 533

; TYPE: PRT

; ORGANISM: Oryza sativa

US-10-449-902-47361

Query Match 20.6%; Score 433; DB 6; Length 533;

Best Local Similarity 28.6%; Pred. No. 7.8e-15;

Matches 124; Conservative 68; Mismatches 146; Indels 96; Gaps 16;

Qy 11 PAPAPP-----PQPP-----TPALPHPPAQP-----PPPPQ-----FPQHVKSGLQIK 51

Db 29 PAQTTPSYNHPQPPPPAEVRYTPSAMNPVPPVPPVAPPKPTPTILGKPYDDVRVYVYLG 88

Qy 52 KNAIDDDYKVTQVLGGLGKGVQIFNKRKTQEKFKALMLQ-----DCPKARREVEL 103

Db 89 KE-----LGRGQFGVYTLCTEIASGKQVACKSISKRLKVSADKEDIRREIQI 136

Qy 104 HWRASQCPHIVRIVYENLYAGRKCLLIVMECLDGGELFSRIQDRGQDAFTEREASEIM 163

Db 137 MQHLSQQNIIVEFRGAYED---KSNVHVVMELCAGGELFDRIIAKGH---YSEAAAAATC 190

Qy 164 KSIGEAIQYLHSINIAHRRDVKPENLLYTSKRPNAILKLITDFG---PAKETTSNLSLTPC 220

Db 191 RAVNVVNTCHFMGVNHRDLKPENFLATKEENAMLKADFGLSVIEGKMYRDIWG-- 248

Qy 221 YTPYVVAPEVLGPEKYDKSCDMSLGVIMVILCGYPPFVSNHGLAISPGMKTRIRMGQY 280

Db 249 -SAYVVAPEVL-RRNYGKEIDVWSAGVILYLLSGVPPFWAE---TEKGIFDAILQGEI 302

Qy 281 EFPNPESVSEVSKMLIRNLKTEPTQRTMTITERMHPWIMOSTKVQPTPLHTSRVLKE 340

Db 303 DFESQWPSPISSEAKDLVRKMLTQDPKRIITSAQVLQHPW-LRDGEASDKPI-DSAVLSR 360

Qy 341 DKE-----RWEDVK-----EEMTSALATMRVD 362

Db 361 MKQFRAMNKLKVALKVIASNLNEEIKGLKQMTNMDTNSGTIYEELKAGLAKLSK 420

Qy 363 YEQIKIKKIEDASN 376

Db 421 LSAEVKQLMEARD 434

RESULT 14

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; GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.

; APPLICANT: Bio-oriented Technology Research Advancement Institution.

; APPLICANT: The Institute of Physical and Chemical Research.

; APPLICANT: Foundation for Advancement of International Science.

; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF





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